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(54) Title: PNI MICROARRAY AND USES

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PNI MICROARRAY AND USES

I. BACKGROUND OF THE INVENTION

- 1. One of the challenges encountered in the design of clinical studies of complex diseases, particularly those with a neurological component, is obtaining informative samples. Even the most cooperative subjects are reluctant to provide neurological samples, and collecting such samples at multiple time-points is simply not feasible. In contrast, peripheral blood is a readily available clinical sample. Many studies have assayed peripheral blood for specific hormones (both peptide and steroid), antibodies, or serum proteins, forming the basis of the understanding of the ongoing communication between the nervous, endocrine, and immune systems.
- 2. This sort of analysis is unfortunately confounded by the fact that most neurotransmitters and hormones are produced and act at sites distinct from the peripheral blood. Also, the microenvironment of the brain is protected by the blood-brain barrier, a lipid membrane that is formed by tight junctions between endothelial cells lining blood vessels in the brain. This barrier allows transport of gases and, by facilitated diffusion, metabolically necessary molecules such as glucose and amino acids. It excludes most large molecules and cells, both bacterial and immune, under normal conditions (Paulson, 2002).

II. SUMMARY OF THE INVENTION

- 3. In accordance with the purposes of this invention, as embodied and broadly described herein, this invention, in one aspect, relates to psychoneuroendocrinimmune (PNI) microarrays.
- 4. Additional advantages of the invention will be set forth in part in the description which follows, and in part will be obvious from the description, or can be learned by practice of the invention. The advantages of the invention will be realized and attained by means of the elements and combinations particularly pointed out in the appended claims. It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed.

III. BRIEF DESCRIPTION OF THE DRAWINGS

5. The accompanying drawings, which are incorporated in and constitute a part of this specification, illustrate several embodiments of the invention and together with the description, serve to explain the principles of the invention.

6. Figure 1 shows the hypothalamus-pituitary-adrenal HPA axis that is vital to appropriate pscyhoneuroendocrinimmune (PNI) response. The complex feedback loop is simplified here to demonstrate the basic components of the HPA axis. The paraventricular nucleus (PVN) of the Hypothalamus secretes corticotropin releasing factor (CRF), also known as corticotropin releasing hormone (CRH), in response to various stressors. This stimulates the corticotrope of the pituitary to release adrenocorticotropic hormone (ACTH), which then acts on the adrendal fasciculata of the adrendals to release of glucocorticoid hormones, such as cortisol. Cortisol completes the feedback loop by inhibiting the release of CRF and ACTH.

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- 7. Figure 2 shows the Composition of an example of the present PNI microarray. 1451 genes were selected for analysis either because they have known or suspected roles in endocrine (24%), nervous (14%), or immune (40%) systems or because changes in their regulation would affect at least one of those systems (22%).
- 8. Figure 3 shows that Nimblegen Microarrays are compatible with the array technology. Replicates of a) Caski cells or PBMCs show reproducible patterns of gene expression. b) The larger spots on the 85K format are amenable to analysis. Shown is a sample data file from Nimblegen with an Arrayvision overlay in red.
- 9. Figure 4 shows that blood was collected and RNA was isolated using either A standard methods (collection in EDTA tubes; no stabilization; RNA isolation using a guanidinium-based method), or B the PAX gene Blood RNA System (for RNA stabilization and isolation). The graphs show changes in expression of 12 genes after blood collection, measured using real-time RT-PCR. Source Precision Medicine, Boulder, Colorado, USA.) (Figure & Text from Qiagen Website)
- 10. Figure 5 shows that bioinformatic analysis reveals that many psychoneuroendocrinimmune genes are expressed in peripheral blood. A) 1451 genes were selected for analysis either because they have known or suspected roles in endocrine (24%), nervous (14%), or immune (40%) systems or because changes in their regulation would affect at least one of those systems (other; 22%). B) 505 of the selected genes were represented by expressed sequence tags (ESTs) in a database constructed from nine blood-derived EST libraries. As expected, a large proportion of these were genes encoding immune system proteins (52%), or classified as "other" (26%), but genes encoding proteins with endocrine (17%) or (5%) nervous system functions were also detected in peripheral blood.

11. Figure 6A shows 1451 genes were selected for analysis either because they have known or suspected roles in endocrine (24%), nervous (14%), or immune (40%) systems or because changes in their regulation would affect at least one of those systems (other; 22%). Figure 6B shows that 505 of the selected genes were represented by expressed sequence tags (ESTs) in a database constructed from nine blood-derived EST libraries. As expected, a large proportion of these were genes encoding immune system proteins (52%), or classified as "other" (26%), but genes encoding proteins with endocrine (17%) or (5%) nervous system functions were predicted to be detectable in peripheral blood.

12. Figure 7 shows an example of a microarray layout.

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- 13. Figure 8 shows an example of a microarray plate design.
- 14. Figure 9 shows the dilutions for the exemplified microarray.
- 15. Figure 10 shows the genes used in the exemplified microarray and their GenBank® accession numbers. Genes were categorized by system and a count of the total number of genes per system and the relative percentage is given.
 - 16. Figure 11 shows the raw data achieved from the microarray.
- 17. Figure 12 shows an analysis of the raw data in particular revealing the differential expression of various genes.
- 18. Figure 13 shows the development of the PNI gene list: Information from a variety of sources was consolidated (A) and the resulting genes were categorized (B). Genes that are categorized as "other" encode proteins with known roles in several of the systems.
- 19. Figure 14 shows that the expression of 301 PNI genes in peripheral blood was verified by both Microarray data and the presence of matching sequences in an EST database derived from cDNAs isolated in blood. Evidence for expression of additional PNI genes was found either by microarray alone (511) or by matching ESTs alone (214). 51 genes indicated by the EST data to be expressed in blood had no detectable expression on the microarray. In this figure, expression by microarray for a given gene is confirmed when at least 75% of the features have a signal-to-noise ratio greater than 2.5.
- 20. Figure 15 shows that approximately 10 percent of genes were never expressed, a small number are expressed by only a few subjects, and the bulk of the genes are expressed by most or all of the subjects. A uniform distribution would have

raised concerns about the 75% cut-off value used in figure 2. The observed distribution instead suggests that individual variability will not be a confounding factor for gene expression profiling using peripheral blood. Also, it was possible that distributions would differ between the categories of genes. However, the proportion of genes expressed in none, some, or all of twenty microarrays prepared using PBMC-derived mRNA was similar for genes categorized as Neuronal or Endocrine as it was for genes categorized as Immune. This is additional evidence that expression of Neuronal or Endocrine genes in blood is meaningful, and suggests it will be possible to use blood to examine the status of an individual's overall PNI functioning.

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- 21. Figure 16 shows scatterplot matrices and Pearson's correlations using log2 Normalized sARM data extracted using Arrayvision. The data has been "deconvoluted", so each point represents a comparison of a specific probe on one replicate array with the corresponding probe on another array, regardless of their actual geographic position. Additionally, probes where the sARMdens/background ratio was less than 2.5 for all three replicates were excluded (approx 30% of probes).
- 22. Figure 17 shows Ranges (in bold) and box plots (in black) of log2 transformed sARM signal intensity for each of the three replicate PNI arrays. The grand mean is denoted by the dotted gray line Blanks are excluded.

IV. DETAILED DESCRIPTION

23. The present invention can be understood more readily by reference to the following detailed description of preferred embodiments of the invention and the Examples included therein and to the Figures and their previous and following description.

24. Before the present compounds, compositions, articles, devices, and/or methods are disclosed and described, it is to be understood that this invention is not limited to specific synthetic methods, specific recombinant biotechnology methods unless otherwise specified, or to particular reagents unless otherwise specified, as such can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting.

A. Definitions

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25. As used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a pharmaceutical carrier" includes mixtures of two or more such carriers, and the like.

- 26. Ranges may be expressed herein as from "about" one particular value, and/or to "about" another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly, when values are expressed as approximations, by use of the antecedent "about," it will be understood that the particular value forms another embodiment. It will be further understood that the endpoints of each of the ranges are significant both in relation to the other endpoint, and independently of the other endpoint.
- 27. In this specification and in the claims which follow, reference will be made to a number of terms which shall be defined to have the following meanings:
- 28. "Optional" or "optionally" means that the subsequently described event or circumstance may or may not occur, and that the description includes instances where said event or circumstance occurs and instances where it does not.
- 29. "Primers" are a subset of probes which are capable of supporting some type of enzymatic manipulation and which can hybridize with a target nucleic acid such that the enzymatic manipulation can occur. A primer can be made from any combination of nucleotides or nucleotide derivatives or analogs available in the art which do not interfere with the enzymatic manipulation.
- 30. "Probes" are molecules capable of interacting with a target nucleic acid, typically in a sequence specific manner, for example through hybridization. The hybridization of nucleic acids is well understood in the art and discussed herein. Typically a probe can be made from any combination of nucleotides or nucleotide derivatives or analogs available in the art. For the purposes of microarrays discussed herein, a "probe" is the tethered nucleic acid with known sequence, whereas a "target" is the free nucleic acid sample whose identity/abundance is being detected.

B. Microarrays

31. Due to the complexity of PNI interactions occurring between immune, endocrine, and nervous systems, assays for one or a few biomolecular markers can be uninformative or misleading. Accordingly, diseases that are characterized by

disturbances in PNI homeostasis or response are among the most significant research and clinical challenges. Gene expression profiling of the most readily available clinical sample, peripheral blood, can be informative in characterizing PNI dysfunction. A bioinformatic analysis of peripheral blood expression of 1451 PNI genes, selected with the intention of elucidating biological pathways, supports this view and its application with other or additional genes. Implications of peripheral blood expression of the PGRMC1 hormone receptor, the hormone responsive protein ZNF147, and several (GABA)ergic system proteins are discussed in detail. Herein disclosed are microarrays comprising genes involved in pscyhoneuroendocrinimmune (PNI) activity.

1. Chips and microarrays

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- 32. Herein an "array," "microarray," or "DNA chip" refers to an orderly arrangement of probes that provides a medium for matching known and unknown DNA samples and automated process of identifying the unknowns. An array experiment can make use of microplates or standard blotting membranes, and can be created by hand or make use of robotics to deposit the probes. Typically, arrays are described as macroarrays or microarrays. Macroarrays contain sample spot sizes of about 300 microns or larger. The sample sizes in microarray are 300 or less microns but typically less than 200 microns in diameter. Microarrays can utilize specialized robotics and/or imaging equipment to enhance throughput and visualization of data. Terminologies that have been used in the literature to describe this technology include, but not limited to: biochip, DNA chip, DNA microarray, GeneChip® (Affymetrix, Inc., which refers to its high density, oligonucleotide-based DNA arrays), and gene array.
- 33. DNA microarrays or DNA chips are generally fabricated on glass but can be made on nylon substrates or other membranes. An experiment with a single DNA chip can provide researchers information on thousands of genes simultaneously. It is herein contemplated that the disclosed microarrays can be used for gene expression monitoring, disease diagnosis, gene discovery, drug discovery (pharmacogenomics), and toxicological research or toxicogenomics which is the hybridization of functional genomics and molecular toxicology.
- 34. Two variants of the DNA microarray technology, in terms of the property of arrayed DNA sequence with known identity are known to exist:

Format I: probe cDNA (500~5,000 bases long) can be immobilized to a solid surface such as glass using robot spotting and exposed to a set of targets

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either separately or in a mixture and is typically referred to as "DNA microarray."

Format II: Called "DNA chips," this format comprises an array of oligonucleotide (20~80-mer oligos) or peptide nucleic acid (PNA) probes is synthesized either in situ or by conventional synthesis followed by immobilization. Labeled sample DNA is then hybridized to the array, and the identity/abundance of complementary sequences are determined.

- 35. The basic concept behind the use of DNA microarrays or DNA chips for gene expression is well known in the art. Typically, labeled cDNA or cRNA targets derived from the mRNA of an experimental sample are hybridized to nucleic acid probes attached to the solid support. By monitoring the amount of label associated with each DNA location, the abundance of each mRNA species represented can be determined.
- 36. The manufacture of DNA microarrays uses photolithography and solid-phase chemistry to produce arrays containing hundreds of thousands of oligonucleotide probes packed at extremely high densities. The probes are designed to maximize sensitivity, specificity, and reproducibility, allowing consistent discrimination between specific and background signals, and between closely related target sequences.
- 37. DNA microarray manufacturing can start with a quartz wafer. Initially the quartz is washed to ensure uniform hydroxylation across its surface. Because quartz is naturally hydroxylated, it provides an excellent substrate for the attachment of chemicals, such as linker molecules, that are later used to position the probes on the arrays.
- 38. The wafer is placed in a bath of silane, which reacts with the hydroxyl groups of the quartz, and forms a matrix of covalently linked molecules. The distance between these silane molecules determines the probes' packing density, allowing arrays to hold over 500,000 probe locations, or features.
- 39. Probe synthesis occurs in parallel, resulting in the addition of an A, C, T, or G nucleotide to multiple growing chains simultaneously. To define which oligonucleotide chains will receive a nucleotide in each step, photolithographic masks, carrying 18 to 20 square micron windows that correspond to the dimensions of individual features, are placed over the coated wafer. The windows are distributed over the mask based on the desired sequence of each probe. When ultraviolet light is shone

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over the mask in the first step of synthesis, the exposed linkers become deprotected and are available for nucleotide coupling.

- 40. Once the desired features have been activated, a solution containing a single type of deoxynucleotide with a removable protection group is flushed over the wafer's surface. The nucleotide attaches to the activated linkers, initiating the synthesis process.
- 41. Although each position in the sequence of an oligonucleotide can be occupied by 1 of 4 nucleotides, resulting in an apparent need for 25 x 4, or 100, different masks per wafer, the synthesis process can be designed to significantly reduce this requirement. It is understood and herein contemplated that algorithms can be used to help minimize mask usage and calculate how to best coordinate probe growth by adjusting synthesis rates of individual probes and identifying situations when the same mask can be used multiple times.
- 42. Some of the key elements of selection and design are common to the production of all DNA microarrays, regardless of their intended application. Strategies to optimize probe hybridization, for example, are invariably included in the process of probe selection. Hybridization under particular pH, salt, and temperature conditions can be optimized by taking into account melting temperatures and using empirical rules that correlate with desired hybridization behaviors.
- 43. To obtain a complete picture of a gene's activity, some probes are selected from regions shared by multiple splice or polyadenylation variants. In other cases, unique probes that distinguish between variants are favored. Inter-probe distance is also factored into the selection process. Probes are 3'-biased to match the target generation characteristics of this sample amplification method, but they are also widely spaced to sample various regions of each transcript and provide robustness of detection.
- 44. A different set of strategies is used to select probes for genotyping arrays that rely on multiple probes to interrogate individual nucleotides in a sequence. The identity of a target base can be deduced using four identical probes that vary only in the target position, each containing one of the four possible bases.
 - 45. Alternatively, the presence of a consensus sequence can be tested using one or two probes representing specific alleles. To genotype heterozygous or genetically mixed samples, arrays with many probes can be created to provide redundant information, resulting in unequivocal genotyping. In addition, generic probes can be used in some applications to maximize flexibility. Some probe arrays, for example,

allow the separation and analysis of individual reaction products from complex mixtures, such as those used in some protocols to identify single nucleotide polymorphisms (SNPs).

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46. Immobilized on a plurality of defined regions of the substrate's surface, are localized multiple copies of one or more polynucleotide sequences, preferably copies of a single polynucleotide sequence. A polynucleotide refers to a chain of nucleotides ranging from 5 to 10,000 nucleotides.

47. The plurality of defined regions on the substrate can be arranged in a variety of formats. For example, the regions may be arranged perpendicular or in parallel to the length of the casing. These immobilized copies of a polynucleotide sequence are suitable for use as a target polynucleotide in hybridization experiments. Furthermore, the probes do not have to be directly bound to the substrate, but rather can be bound to the substrate through a linker group. The linker groups may typically vary from about 6 to 50 atoms long. Preferred linker groups include ethylene glycol oligomers, diamines, diacids and the like. Reactive groups on the substrate surface react with one of the terminal portions of the linker to bind the linker to the substrate. The other terminal portion of the linker is then functionalized for binding the polynucleotides.

48. To prepare beads coated with immobilized polynucleotide sequences, beads are immersed in a solution containing the desired polynucleotide sequence and then immobilized on the beads by covalent or noncovalent means. Alternatively, when the polynucleotides are immobilized on rods, a given polynucleotide can be spotted at defined regions of the rod. Typical dispensers include a micropipette delivering solution to the substrate with a robotic system to control the position of the micropipette with respect to the substrate. There can be a multiplicity of dispensers so that reagents can be delivered to the reaction regions simultaneously. In one embodiment, a microarray is formed by using ink-jet technology based on the piezoelectric effect, whereby a narrow tube containing a liquid of interest, such as oligonucleotide synthesis reagents, is encircled by an adapter. An electric charge sent across the adapter causes the adapter to expand at a different rate than the tube and forces a small drop of liquid onto a substrate (Baldeschweiler et al. PCT publication WO95/251116).

49. Samples may be any sample containing polynucleotides (polynucleotide probes) of interest and obtained from any bodily fluid (blood, urine, saliva, phlegm,

gastric juices, etc.), cultured cells, biopsies, or other tissue preparations. DNA or RNA can be isolated from the sample according to any of a number of methods well known to those of skill in the art. For example, methods of purification of nucleic acids are described in Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes. Part I. Theory and Nucleic Acid Preparation, P. Tijssen, ed. Elsevier (1993). In. a preferred embodiment, total RNA is isolated using the TRIzol total RNA isolation reagent (Life Technologies, Inc., Rockville, Md.) and RNA is isolated using oligo d(T) column chromatography or glass beads. After hybridization and processing, the hybridization signals obtained should reflect accurately the amounts of control target polynucleotide added to the sample.

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- 50. Sample polynucleotides may be labeled with one or more labeling moieties to allow for detection of hybridized probe/target polynucleotide complexes. The labeling moieties can include compositions that can be detected by spectroscopic, photochemical, biochemical, bioelectronic, immunochemical, electrical, optical or chemical means. The labeling moieties include radioisotopes, such as .sup.32 P, .sup.33 P or .sup.35 S, chemiluminescent compounds, labeled binding proteins, heavy metal atoms, spectroscopic markers, such as fluorescent markers and dyes, magnetic labels, linked enzymes, mass spectrometry tags, spin labels, electron transfer donors and acceptors, biotin, and the like.
- 51. Labeling can be carried out during an amplification reaction, such as polymerase chain reaction and in vitro or in vivo transcription reactions. Alternatively, the labeling moiety can be incorporated after hybridization once a probe-target complex his formed. In one preferred embodiment, biotin is first incorporated during an amplification step as described above. After the hybridization reaction, unbound nucleic acids are rinsed away so that the only biotin remaining bound to the substrate is that attached to target polynucleotides that are hybridized to the polynucleotide probes. Then, an avidin-conjugated fluorophore, such as avidin-phycoerythrin, that binds with high affinity to biotin is added.
- 52. Hybridization causes a polynucleotide probe and a complementary target to form a stable duplex through base pairing. Hybridization methods are well known to those skilled in the art. Stringent conditions for hybridization can be defined by salt concentration, temperature, and other chemicals and conditions. Varying additional parameters, such as hybridization time, the concentration of detergent (sodium dodecyl

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sulfate, SDS) or solvent (formamide), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Additional variations on these conditions will be readily apparent to those skilled in the art (Wahl, G. M. and S. L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A. R. (1987) Methods Enzymol. 152:507-511; Ausubel, F. M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y.; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y.).

- 53. Methods for detecting complex formation are well known to those skilled in the art. In a preferred embodiment, the polynucleotide probes are labeled with a fluorescent label and measurement of levels and patterns of complex formation is accomplished by fluorescence microscopy, preferably confocal fluorescence microscopy. An argon ion laser excites the fluorescent label, emissions are directed to a photomultiplier and the amount of emitted light detected and quantitated. The detected signal should be proportional to the amount of probe/target polynucleotide complex at each position of the microarray. The fluorescence microscope can be associated with a computer-driven scanner device to generate a quantitative two-dimensional image of hybridization intensities. The scanned image is examined to determine the abundance/expression level of each hybridized target polynucleotide.
- 54. In a differential hybridization experiment, polynucleotide probes from two or more different biological samples are labeled with two or more different fluorescent labels with different emission wavelengths. Fluorescent signals are detected separately with different photomultipliers set to detect specific wavelengths. The relative abundances/expression levels of the target polynucleotides in two or more samples is obtained. Typically, microarray fluorescence intensities can be normalized to take into account variations in hybridization intensities when more than one microarray is used under similar test conditions. Individual polynucleotide probe/target complex hybridization intensities can be normalized using the intensities derived from internal normalization controls contained on each microarray.
- 55. The two cDNA probes are tested by hybridizing them to a DNA microarray. The array holds hundreds or thousands of spots, each of which contains a different DNA sequence. If a probe contains a cDNA whose sequence is complementary to the DNA on a given spot, that cDNA will hybridize to the spot, where it will be detectable by its fluorescence. In this way, every spot on an array is an independent assay for the

presence of a different cDNA. There is enough DNA on each spot that both probes can hybridize to it at once without interference.

2. PNI

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56. Psychoneuroendocrinimmune functions refer to the interplay of the endocrine, immune, and neuronal systems to maintain a level of stasis within an individual or subject. PNI gene expression is substantially mediated by the hypothalamus-pituitary-adrenal (HPA) axis. Dysregulation of this axis and thus PNI is associated with a variety of diseases and conditions including inflammatory conditions, cancers, and infectious diseases such as viral and bacterial infections. Because of the diverse nature of the systems involved in PNI function, determining the role PNI plays in a condition and determining the role genes of the various systems play in PNI has been difficult prior to the invention disclosed herein.

57. Herein disclosed are microarrays comprising probes for genes involved in pscyhoneuroendocrinimmune (PNI) activity. Thus, for example, specifically disclosed are microarrays in which the probes are selected to identify the group of genes which can be identified by hybridization to the gene or gene fragments (e.g., ESTs) consisting of SEQ ID NOS: 1-1741 and 3086-3314. These are examples of human gene probes for use in the present microarray. Also disclosed are microarrays in which the genes are selected from the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514. This is a mouse miroarray. It is understood and herein contemplated that microarrays consisting of a subset of the PNI genes disclosed herein can be made. Therefore, specifically disclosed are microarrays of the invention, wherein the array consists of 100 of the human genes selected from the group of PNI associated genes consisting of SEQ ID NO: 1-3514. Also disclosed are microarrays consisting of 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, or 1622 or any number in between of the genes selected from the group of human PNI associated genes consisting of SEQ ID NO: 1-3514. Thus, for example, specifically disclosed is a microarray of the invention, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1-1741 and 3086-3314, and wherein the number of genes selected is 1969. Also disclosed is a microarray of the invention, wherein the genes are selected from the the group of mouse genes consisting of SEQ ID NO: 1742-3085 and 3315-3514, and wherein the number of genes selected is 100. Also disclosed are microarrays consisting of 200, 300, 400, 500, 600, 700, 800, 900, 1000,

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1100, 1200, 1300, 1400 or 1542 or any number in between of the genes selected from the group of mouse PNI associated genes consisting of SEQ ID NO: 1-3514.

- 58. Typically microarrays comprise genes other than those of interest (e.g. PNI associated genes) for purposes of establishing controls for level of gene expression or to monitor the array itself. Such genes are often referred to as housekeeping genes. Control genes can also comprise SEQ ID NOs: 3534-3685. Arabidopsis genes can serve as positive controls for gene expression. Such genes are shown in SEQ ID NO: 3515-3533. It is understood that the specific control genes are not crucial to the microarray and can be exchanged for any equivalent control gene. It is understood that those of skill in the art know which genes can be substituted for the control genes disclosed herein. Thus, specifically disclosed are microarrays of the invention further comprising housekeeping or other control genes. For example, specifically disclosed are microarrays of the invention further comprising genes selected from the group of genes consisting of SEQ ID NOs: 3515-3685.
- 59. Disclosed are chips where at least one location (address) is the sequences or part of the sequences set forth in any of the nucleic acid sequences disclosed herein.

 Also disclosed are chips where at least one address is the sequences or portion of sequences set forth in any of the peptide sequences disclosed herein.
- 60. Also disclosed are chips where at least one address is a variant of the sequences or part of the sequences set forth in any of the nucleic acid sequences disclosed herein. Also disclosed are chips where at least one address is a variant of the sequences or portion of sequences set forth in any of the peptide sequences disclosed herein.

3. Methods of using the microarrays to diagnose a condition

61. The disclosed microarrays have many uses. One such use can relate to diagnosing conditions associated with PNI activity. Therefore, specifically disclosed and herein contemplated are methods for diagnosing a condition associated with PNI activity comprising obtaining a sample from a subject, isolating RNA from the sample, placing the RNA on a PNI microarray, and analyzing the gene expression on the array. Genes and conditions associated with PNI activity have a role in multiple systems in a body and can present a variety of symptoms. It is understood for example that the disclosed methods can be used for conditions, wherein the condition is selected from the group of PNI associated conditions consisting of CFS, type-2 diabetes, allergic

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conditions including atopic dermatitis, rheumatic diseases such as rheumatoid arthritis and systemic lupus erythematosus, Sjogren's syndrome, coronary heart disease, inflammatory bowel disease, acute depression, fatigue diseases resulting from defined causes, such as cancer treatment, post traumatic stress disease, susceptibility to alcoholism, Alzheimer's Disease, and cognitive impairment resulting from multiple sclerosis.

- 62. Also disclosed are diagnositic methods, wherein the condition is an inflammatory condition. It is understood and herein contemplated that inflammatory conditions can also comprise autoimmune diseases as well as allergic reactions. Thus, for example, specifically disclosed are diagnostic methods of the invention, wherein the inflammatory condition is selected from the group of inflammatory conditions consisting of asthma, alopecia areata, systemic lupus erythematosus, rheumatoid arthritis, reactive arthritis, spondylarthritis, systemic vasculitis, insulin dependent diabetes mellitus, multiple sclerosis, experimental allergic encephalomyelitis, Sjögren's syndrome, graft versus host disease, inflammatory bowel disease including Crohn's disease, ulcerative colitis, ischemia reperfusion injury, myocardial infarction, Alzheimer's disease, transplant rejection (allogeneic and xenogeneic), thermal trauma, any immune complex-induced inflammation, glomerulonephritis, myasthenia gravis, cerebral lupus, Guillain-Barre syndrome, vasculitis, systemic sclerosis, anaphlaxis, catheter reactions, atheroma, infertility, thyroiditis, ARDS, post-bypass syndrome, hemodialysis, juvenile rheumatoid, Behcets syndrome, hemolytic anemia, pemphigus, bullous pemphigoid, stroke, atherosclerosis, scleroderma, psoriasis, sarcoidosis, transverse myelitis, acute disseminated encephalomyelitis, post-infectious encephalomyelitis, subacute sclerosing panencephalitis, and chronic inflammatory demyelinating polyradiculopathy.
- 63. It is understood that the present methods disclosed herein can be used with conditions, wherein the condition is a cancer. Thus, specifically disclosed are methods for diagnosing a condition associated with PNI activity comprising obtaining a tissue sample from a subject, isolating RNA from the sample, placing the RNA on a PNI microarray, and analyzing the gene expression on the array, wherein the cancer is selected from the group of cancers consisting of lymphoma, B cell lymphoma, T cell lymphoma, mycosis fungoides, Hodgkin's Disease, myeloid leukemia, bladder cancer, brain cancer, nervous system cancer, head and neck cancer, squamous cell carcinoma

of head and neck, kidney cancer, lung cancers such as small cell lung cancer and non-small cell lung cancer, neuroblastoma/glioblastoma, ovarian cancer, pancreatic cancer, prostate cancer, skin cancer, liver cancer, melanoma, squamous cell carcinomas of the mouth, throat, larynx, and lung, colon cancer, cervical cancer, cervical carcinoma, breast cancer, and epithelial cancer, renal cancer, genitourinary cancer, pulmonary cancer, esophageal carcinoma, head and neck carcinoma, large bowel cancer, hematopoietic cancers; testicular cancer; colon and rectal cancers, prostatic cancer, or pancreatic cancer.

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- 64. Infectious diseases are conditions associated with a bacterial, viral, fungal, or parasitic infection. Such diseases result in the expression of multiple genes from a variety of systems either through the direct action of the infecting pathogen or as a result of the hosts response to the presence of the pathogen. Thus specifically disclosed are methods for diagnosing a condition associated with PNI activity comprising obtaining a tissue sample from a subject, isolating RNA from the sample, placing the RNA on a PNI microarray, and analyzing the gene expression on the array, wherein the infectious disease is a bacterial infection selected from the group of bacteria consisting of M. tuberculosis, M. bovis, M. bovis strain BCG, BCG substrains, M. avium, M. intracellulare, M. africanum, M. kansasii, M. marinum, M. ulcerans, M. avium subspecies paratuberculosis, Nocardia asteroides, other Nocardia species, Legionella pneumophila, other Legionella species, Salmonella typhi, other Salmonella species, Shigella species, Yersinia pestis, Pasteurella haemolytica, Pasteurella multocida, other Pasteurella species, Actinobacillus pleuropneumoniae, Listeria monocytogenes, Listeria ivanovii, Brucella abortus, other Brucella species, Cowdria ruminantium, Chlamydia pneumoniae, Chlamydia trachomatis, Chlamydia psittaci, Coxiella burnetti, other Rickettsial species, Ehrlichia species, Staphylococcus aureus, Staphylococcus epidermidis, Streptococcus pyogenes, Streptococcus agalactiae, Bacillus anthracis, Escherichia coli, Vibrio cholerae, Campylobacter species, Neiserria meningitidis, Neiserria gonorrhea, Pseudomonas aeruginosa, other Pseudomonas species, Haemophilus influenzae, Haemophilus ducreyi, other Hemophilus species, Clostridium tetani, other Clostridium species, Yersinia enterolitica, and other Yersinia species.
- 65. Also disclosed are the diagnostic methods of the invention, wherein the infectious disease is a viral infection selected from the group of viruses consisting of Herpes simplex virus type-1, Herpes simplex virus type-2, Cytomegalovirus, Epstein-

Barr virus, Varicella-zoster virus, Human herpesvirus 6, Human herpesvirus 7, Human herpesvirus 8, Variola virus, Vesicular stomatitis virus, Hepatitis A virus, Hepatitis B virus, Hepatitis C virus, Hepatitis D virus, Hepatitis E virus, Rhinovirus, Coronavirus, Influenza virus A, Influenza virus B, Measles virus, Polyomavirus, Human Papilomavirus, Respiratory syncytial virus, Adenovirus, Coxsackie virus, Dengue 5 virus, Mumps virus, Poliovirus, Rabies virus, Rous sarcoma virus, Yellow fever virus, Ebola virus, Marburg virus, Lassa fever virus, Eastern Equine Encephalitis virus, Japanese Encephalitis virus, St. Louis Encephalitis virus, Murray Valley fever virus, West Nile virus, Rift Valley fever virus, Rotavirus A, Rotavirus B, Rotavirus C, Sindbis virus, Simian Immunodeficiency cirus, Human T-cell Leukemia virus type-1, 10 Hantavirus, Rubella virus, Simian Immunodeficiency virus, Human Immunodeficiency virus type-1, and Human Immunodeficiency virus type-2.

66. Also disclosed are the diagnostic methods of the invention, wherein the infectious disease is a fungal infection selected from the group of fungi consisting of Candida albicans, Cryptococcus neoformans, Histoplama capsulatum, Aspergillus fumigatus, Coccidiodes immitis, Paracoccidiodes brasiliensis, Blastomyces dermitidis, Pneomocystis carnii, Penicillium marneffi, and Alternaria alternata.

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67. Also disclosed are the diagnostic methods of the invention, wherein the infectious disease is a parasitic infection selected from the group of parasites consisting of Toxoplasma gondii, Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae, other Plasmodium species, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, other Leishmania species., Schistosoma mansoni, other Schistosoma species., and Entamoeba histolytica.

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68. It is understood that the disclosed microarrays can be used to compile vast databases of the genetic profiles of subjects with a condition associated with PNI activity. Such databases can then be used to establish known genes associated with a particular condition. If using a microarray of the invention, a particular pattern of gene expression of the array itself can be use to identify a pattern associated with a disease state. Such a pattern can be to diagnose a particular condition. Thus also disclosed are diagnostic methods, further comprising making a diagnosis based on the pattern of gene expression on the microarray, wherein a pattern matching one associated with a condition indicates the subject has the condition.

69. The present methods utilize tissue samples as a source of RNA for the microarray samples. As used herein, "tissue sample" refers to any cell, tissue, or organ from a multicellular organism, including but not limited to, blood, neuronal tissue, organ biopsy, lung lavage, sputum, lymph, and excretory waste.

70. The methods disclosed herein often utilize subjects to obtain tissue samples or as a target for diagnosis. It is understood that herein a subject can refer to any mammalian organism including but not limited to mouse, rat, guinea pig, rabbit, dog, cat, pig, horse, cow, monkey, chimpanzee, and human.

4. Computer readable mediums

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- 71. It is understood that the disclosed nucleic acids and proteins can be represented as a sequence consisting of the nucleotides or amino acids. There are a variety of ways to display these sequences, for example the nucleotide guanosine can be represented by G or g. Likewise the amino acid valine can be represented by Val or V. Those of skill in the art understand how to display and express any nucleic acid or protein sequence in any of the variety of ways that exist, each of which is considered herein disclosed. IUPAC symbols provide a convenient, scientifically accepted way to nucleotide or amino acid identification information. Specifically contemplated herein is the display of these sequences on computer readable mediums, such as, commercially available floppy disks, tapes, chips, hard drives, compact disks, and video disks, or other computer readable mediums. Also disclosed are the binary code representations of the disclosed sequences. Those of skill in the art understand what computer readable mediums. Thus, computer readable mediums on which the nucleic acids or protein sequences are recorded, stored, or saved.
- 72. Disclosed are computer readable mediums comprising the sequences and information regarding the sequences set forth herein. Also disclosed are computer readable mediums comprising the sequences and information regarding the sequences set forth herein.

5. Methods of evaluating expression of genes using microarrays.

73. Disclosed herein are methods relating to the evaluation of gene expression using microarrays. Methods of evaluating expression of genes involved in PNI using microarrays are provided. Disclosed are methods of identifying genes involved in a condition associated with PNI activity comprising obtaining tissue samples from subjects with the condition and a control population, isolating the RNA, analyzing the

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RNA using a PNI microarray, and comparing the expression of genes in the subjects with the condition to the control population. In this analysis, a variety of known algorithms can be applied based on, for example, an experimental result in which gene expression present in 70% or more of the subjects with a diagnosed condition, but in fewer than 20% of the controls without the condition indicates genes involved in a condition associated with PNI activity. Additionally, algorithms relevant to a particular condition can be developed based on the data obtained using the present PNI microarray for a particular condition. These can then be applied to data from unknown subjects.

74. Disclosed are methods of classifying a condition as being associated with PNI activity comprising obtaining tissue samples from subjects with the condition and a control population, isolating the RNA, analyzing the RNA using a PNI microarray, and comparing the expression of genes in the subjects with the condition to the control population, wherein conditions that result in gene expression present in 70% or more of the subjects, but in fewer than 20% of the controls indicates a condition associated with PNI activity.

6. Computer implemented methods of diagnosing PNI diseases by gene expression profile comparison.

75. Disclosed are computer implemented methods of receiving patient PNI microarray gene expression data, creating a gene expression profile from said data, comparing patient gene expression profile to known PNI disease gene expression profiles, and diagnosing patient condition based on percent similarity to known PNI disease gene expression profiles. Also disclosed are methods of analyzing microarrays using computer readable mediums. It is understood and herein contemplated that technological advances have enabled researchers to study overall patterns in gene expression. This is significant, as these patterns provide the context for specific observations. For certain complex diseases, distinctive peripheral blood gene expression patterns have been characterized. For example, herein discosed, individuals with chronic fatigue syndrome (CFS) were compared with healthy controls by gene expression profiling, and evidence for altered expression of immune and nervous system genes in the CFS patients was found.

76. Such disease gene expression profiles can be used in conjunction with a computer implemented disease diagnosis system. Known disease gene expression

profiles can be stored in a database. These profiles can be stored in a disease gene expression profile table consisting of a column indicating the unique gene identifier and a column indicating the expression level corresponding to the gene. Disease gene expression data can be stored as a range of expression levels or many profiles for an individual disease can be stored. The gene expression data obtained from a PNI microarray for a patient with a possible PNI disease can be stored in a patient experiment table consisting of a column indicating the unique gene identifier and a column indicating the expression level corresponding to the gene. Patient gene expression data can also be stored as a range of expression levels. The patient experiment table can be computationally compared to the disease gene expression profile table. From this comparison a diagnosis and a percent confidence can be calculated based on the similarity between the patient gene expression profile and the known disease gene expression profile. A graphical user interface can be used to make such diagnosis user friendly.

77. Thus specifically disclosed and herein contemplated are computer implemented methods of comparing gene expression profiles for disease diagnosis, the method comprising a) providing a database including a library of known disease gene expression profiles; b) receiving patient gene expression data from PNI microarray; c) converting said patient gene expression data into a gene expression profile; d) comparing patient gene expression profile to known disease gene expression profile library; e) determining percent confidence of patient disease from patient gene expression profile similarity to known disease gene expression profile library; and f) displaying the results of said determination.

78. Also disclosed are systems for diagnosing a disease comprising a database for storing at least one of a plurality of known disease gene expression profiles and a processor for performing the steps of: a) storing a plurality of known disease gene expression profiles; b) receiving patient gene expression data; c) converting patient gene expression data into a patient gene expression profile; d) performing a comparison operation on the plurality of known disease gene expression profiles and the patient gene expression profile to produce a percent confidence corresponding to a known disease; and e) outputting the disease diagnosis and percent confidence on an output device.

7. Methods of screening using a chip/microarray.

79. Disclosed are methods of screening pharmaceutical agents for the ability to modulate genes involved in PNI. In the screening method, a putative modulator of a disease mechanism involving PNI or the HPA axis is administered to an experimental subject whose gene expression is then measured using the present PNI microarray, followed by comparing the gene expression profile to a profile from a similar subject not receiving the putative modulator. A change in the PNI profile of the subject receiving the putative modulator compound indicates that the compound is a modulator of PNI or the HPA axis. Also disclosed are methods of diagnosing subjects with a condition comprising removing a DNA or RNA source sample from the subject and subjecting the sample to a PNI microarray.

C. Compositions

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80. Disclosed are the components to be used to prepare the disclosed compositions as well as the compositions themselves to be used within the methods disclosed herein. These and other materials are disclosed herein, and it is understood that when combinations, subsets, interactions, groups, etc. of these materials are disclosed that while specific reference of each various individual and collective combinations and permutation of these compounds may not be explicitly disclosed, each is specifically contemplated and described herein. For example, if a particular PNI array is disclosed and discussed and a number of modifications that can be made to a number of molecules including the PNI array are discussed, specifically contemplated is each and every combination and permutation of the PNI array and the modifications that are possible unless specifically indicated to the contrary. Thus, if a class of molecules A, B, and C are disclosed as well as a class of molecules D, E, and F and an example of a combination molecule, A-D is disclosed, then even if each is not individually recited each is individually and collectively contemplated meaning combinations, A-E, A-F, B-D, B-E, B-F, C-D, C-E, and C-F are considered disclosed. Likewise, any subset or combination of these is also disclosed. Thus, for example, the sub-group of A-E, B-F, and C-E would be considered disclosed. This concept applies to all aspects of this application including, but not limited to, steps in methods of making and using the disclosed compositions. Thus, if there are a variety of additional steps that can be performed it is understood that each of these additional steps can be

performed with any specific embodiment or combination of embodiments of the disclosed methods.

1. Sequence similarities

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- 81. It is understood that as discussed herein the use of the terms homology and identity mean the same thing as similarity. Thus, for example, if the use of the word homology is used between two non-natural sequences it is understood that this is not necessarily indicating an evolutionary relationship between these two sequences, but rather is looking at the similarity or relatedness between their nucleic acid sequences. Many of the methods for determining homology between two evolutionarily related molecules are routinely applied to any two or more nucleic acids or proteins for the purpose of measuring sequence similarity regardless of whether they are evolutionarily related or not.
- 82. In general, it is understood that one way to define any known variants and derivatives or those that might arise, of the disclosed genes and proteins herein, is through defining the variants and derivatives in terms of homology to specific known sequences. This identity of particular sequences disclosed herein is also discussed elsewhere herein. In general, variants of genes and proteins herein disclosed typically have at least, about 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent homology to the stated sequence or the native sequence. Those of skill in the art readily understand how to determine the homology of two proteins or nucleic acids, such as genes. For example, the homology can be calculated after aligning the two sequences so that the homology is at its highest level.
- 83. Another way of calculating homology can be performed by published algorithms. Optimal alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2: 482 (1981), by the homology alignment algorithm of Needleman and Wunsch, J. MoL Biol. 48: 443 (1970), by the search for similarity method of Pearson and Lipman, Proc. Natl. Acad. Sci. U.S.A. 85: 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by inspection.
 - 84. The same types of homology can be obtained for nucleic acids by for example the algorithms disclosed in Zuker, M. Science 244:48-52, 1989, Jaeger et al.

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Proc. Natl. Acad. Sci. USA 86:7706-7710, 1989, Jaeger et al. Methods Enzymol. 183:281-306, 1989 which are herein incorporated by reference for at least material related to nucleic acid alignment. It is understood that any of the methods typically can be used and that in certain instances the results of these various methods can differ, but the skilled artisan understands if identity is found with at least one of these methods, the sequences would be said to have the stated identity, and be disclosed herein.

85. For example, as used herein, a sequence recited as having a particular percent homology to another sequence refers to sequences that have the recited homology as calculated by any one or more of the calculation methods described above. For example, a first sequence has 80 percent homology, as defined herein, to a second sequence if the first sequence is calculated to have 80 percent homology to the second sequence using the Zuker calculation method even if the first sequence does not have 80 percent homology to the second sequence as calculated by any of the other calculation methods. As another example, a first sequence has 80 percent homology, as defined herein, to a second sequence if the first sequence is calculated to have 80 percent homology to the second sequence using both the Zuker calculation method and the Pearson and Lipman calculation method even if the first sequence does not have 80 percent homology to the second sequence as calculated by the Smith and Waterman calculation method, the Needleman and Wunsch calculation method, the Jaeger calculation methods, or any of the other calculation methods. As yet another example, a first sequence has 80 percent homology, as defined herein, to a second sequence if the first sequence is calculated to have 80 percent homology to the second sequence using each of calculation methods (although, in practice, the different calculation methods will often result in different calculated homology percentages).

2. Hybridization/selective hybridization

86. The term hybridization typically means a sequence driven interaction between at least two nucleic acid molecules, such as a primer or a probe and a gene. Sequence driven interaction means an interaction that occurs between two nucleotides or nucleotide analogs or nucleotide derivatives in a nucleotide specific manner. For example, G interacting with C or A interacting with T are sequence driven interactions. Typically sequence driven interactions occur on the Watson-Crick face or Hoogsteen face of the nucleotide. The hybridization of two nucleic acids is affected by a number of conditions and parameters known to those of skill in the art. For example, the salt

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concentrations, pH, and temperature of the reaction all affect whether two nucleic acid molecules will hybridize.

87. Parameters for selective hybridization between two nucleic acid molecules are well known to those of skill in the art. For example, in some embodiments selective hybridization conditions can be defined as stringent hybridization conditions. For example, stringency of hybridization is controlled by both temperature and salt concentration of either or both of the hybridization and washing steps. For example, the conditions of hybridization to achieve selective hybridization can involve hybridization in high ionic strength solution (6X SSC or 6X SSPE) at a temperature that is about 12-25°C below the Tm (the melting temperature at which half of the molecules dissociate from their hybridization partners) followed by washing at a combination of temperature and salt concentration chosen so that the washing temperature is about 5°C to 20°C below the Tm. The temperature and salt conditions are readily determined empirically in preliminary experiments in which samples of reference DNA immobilized on filters are hybridized to a labeled nucleic acid of interest and then washed under conditions of different stringencies. Hybridization temperatures are typically higher for DNA-RNA and RNA-RNA hybridizations. The conditions can be used as described above to achieve stringency, or as is known in the art. (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989; Kunkel et al. Methods Enzymol. 1987:154:367, 1987 which is herein incorporated by reference for material at least related to hybridization of nucleic acids). A preferable stringent hybridization condition for a DNA:DNA hybridization can be at about 68°C (in aqueous solution) in 6X SSC or 6X SSPE followed by washing at 68°C. Stringency of hybridization and washing, if desired, can be reduced accordingly as the degree of complementarity desired is decreased, and further, depending upon the G-C or A-T richness of any area wherein variability is searched for. Likewise, stringency of hybridization and washing, if desired, can be increased accordingly as homology desired is increased, and further, depending upon the G-C or A-T richness of any area wherein high homology is desired, all as known in the art.

88. Another way to define selective hybridization is by looking at the amount (percentage) of one of the nucleic acids bound to the other nucleic acid. For example, in some embodiments selective hybridization conditions would be when at least about,

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 $60, 65, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100 percent of the limiting nucleic acid is bound to the non-limiting nucleic acid. Typically, the non-limiting primer is in for example, 10 or 100 or 1000 fold excess. This type of assay can be performed at under conditions where both the limiting and non-limiting primer are for example, 10 fold or 100 fold or 1000 fold below their <math>k_d$, or where only one of the nucleic acid molecules is 10 fold or 100 fold or 1000 fold or where one or both nucleic acid molecules are above their k_d .

- 89. Another way to define selective hybridization is by looking at the percentage of primer that gets enzymatically manipulated under conditions where hybridization is required to promote the desired enzymatic manipulation. For example, in some embodiments selective hybridization conditions would be when at least about, 60, 65, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100 percent of the primer is enzymatically manipulated under conditions which promote the enzymatic manipulation, for example if the enzymatic manipulation is DNA extension, then selective hybridization conditions would be when at least about 60, 65, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100 percent of the primer molecules are extended. Preferred conditions also include those suggested by the manufacturer or indicated in the art as being appropriate for the enzyme performing the manipulation.
- 90. Just as with homology, it is understood that there are a variety of methods herein disclosed for determining the level of hybridization between two nucleic acid molecules. It is understood that these methods and conditions can provide different percentages of hybridization between two nucleic acid molecules, but unless otherwise indicated meeting the parameters of any of the methods would be sufficient. For example if 80% hybridization was required and as long as hybridization occurs within the required parameters in any one of these methods it is considered disclosed herein.
- 91. It is understood that those of skill in the art understand that if a composition or method meets any one of these criteria for determining hybridization either collectively or singly it is a composition or method that is disclosed herein.

3. Nucleic acids

92. There are a variety of molecules disclosed herein that are nucleic acid based, including for example the nucleic acids that encode, for example PTPN18, as well as

various functional nucleic acids. The disclosed nucleic acids are made up of for example, nucleotides, nucleotide analogs, or nucleotide substitutes. Non-limiting examples of these and other molecules are discussed herein. It is understood that for example, when a vector is expressed in a cell, that the expressed mRNA will typically be made up of A, C, G, and U. Likewise, it is understood that if, for example, an antisense molecule is introduced into a cell or cell environment through for example exogenous delivery, it is advantagous that the antisense molecule be made up of nucleotide analogs that reduce the degradation of the antisense molecule in the cellular environment.

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a) Nucleotides and related molecules

93. A nucleotide is a molecule that contains a base moiety, a sugar moiety and a phosphate moiety. Nucleotides can be linked together through their phosphate moieties and sugar moieties creating an internucleoside linkage. The base moiety of a nucleotide can be adenin-9-yl (A), cytosin-1-yl (C), guanin-9-yl (G), uracil-1-yl (U), and thymin-1-yl (T). The sugar moiety of a nucleotide is a ribose or a deoxyribose. The phosphate moiety of a nucleotide is pentavalent phosphate. An non-limiting example of a nucleotide would be 3'-AMP (3'-adenosine monophosphate) or 5'-GMP (5'-guanosine monophosphate).

94. A nucleotide analog is a nucleotide which contains some type of modification to either the base, sugar, or phosphate moieties. Modifications to the base moiety would include natural and synthetic modifications of A, C, G, and T/U as well as different purine or pyrimidine bases, such as uracil-5-yl (.psi.), hypoxanthin-9-yl (I), and 2-aminoadenin-9-yl. A modified base includes but is not limited to 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiothymine and

95. 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Additional base modifications can be found for example in U.S. Pat. No. 3,687,808,

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Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613, and Sanghvi, Y. S., Chapter 15, Antisense Research and Applications, pages 289-302, Crooke, S. T. and Lebleu, B. ed., CRC Press, 1993. Certain nucleotide analogs, such as 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine can increase the stability of duplex formation. Often time base modifications can be combined with for example a sugar modification, such as 2'-O-methoxyethyl, to achieve unique properties such as increased duplex stability. There are numerous United States patents such as 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; and 5,681,941, which detail and describe a range of base modifications. Each of these patents is herein incorporated by reference.

96. Nucleotide analogs can also include modifications of the sugar moiety. Modifications to the sugar moiety would include natural modifications of the ribose and deoxy ribose as well as synthetic modifications. Sugar modifications include but are not limited to the following modifications at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl can be substituted or unsubstituted C₁ to C₁₀, alkyl or C₂ to C₁₀ alkenyl and alkynyl. 2' sugar modiifications also include but are not limited to - O[(CH₂)_n O]_m CH₃, -O(CH₂)_n OCH₃, -O(CH₂)_n NH₂, -O(CH₂)_n CH₃, -O(CH₂)_n -ONH₂, and -O(CH₂)_nON[(CH₂)_n CH₃)]₂, where n and m are from 1 to about 10.

97. Other modifications at the 2' position include but are not limted to: C₁ to C₁₀

lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, CF₃, OCF₃, SOCH₃, SO₂ CH₃, ONO₂, NO₂, NO₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. Similar modifications can also be made at other positions on the sugar, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Modified sugars would also include those that contain modifications at the bridging ring oxygen, such as CH₂ and S. Nucleotide sugar analogs can also have sugar mimetics such as cyclobutyl

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moieties in place of the pentofuranosyl sugar. There are numerous United States patents that teach the preparation of such modified sugar structures such as 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5;700,920, each of which is herein incorporated by reference in its entirety.

98. Nucleotide analogs can also be modified at the phosphate moiety. Modified phosphate moieties include but are not limited to those that can be modified so that the linkage between two nucleotides contains a phosphorothioate, chiral phosphorothioate, phosphorodithioate, phosphotriester, aminoalkylphosphotriester, methyl and other alkyl phosphonates including 3'-alkylene phosphonate and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates. It is understood that these phosphate or modified phosphate linkage between two nucleotides can be through a 3'-5' linkage or a 2'-5' linkage, and the linkage can contain inverted polarity such as 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included. Numerous United States patents teach how to make and use nucleotides containing modified phosphates and include but are not limited to, 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; and 5,625,050, each of which is herein incorporated by reference.

99. It is understood that nucleotide analogs need only contain a single modification, but can also contain multiple modifications within one of the moieties or between different moieties.

100. Nucleotide substitutes are molecules having similar functional properties to nucleotides, but which do not contain a phosphate moiety, such as peptide nucleic acid (PNA). Nucleotide substitutes are molecules that will recognize nucleic acids in a Watson-Crick or Hoogsteen manner, but which are linked together through a moiety other than a phosphate moiety. Nucleotide substitutes are able to conform to a double helix type structure when interacting with the appropriate target nucleic acid.

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Nucleotide substitutes are nucleotides or nucleotide analogs that have 101. had the phosphate moiety and/or sugar moieties replaced. Nucleotide substitutes do not contain a standard phosphorus atom. Substitutes for the phosphate can be for example, short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH2 component parts. Numerous United States patents disclose how to make and use these types of phosphate replacements and include but are not limited to 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439, each of which is herein incorporated by reference.

- 102. It is also understood in a nucleotide substitute that both the sugar and the phosphate moieties of the nucleotide can be replaced, by for example an amide type linkage (aminoethylglycine) (PNA). United States patents 5,539,082; 5,714,331; and 5,719,262 teach how to make and use PNA molecules, each of which is herein incorporated by reference. (See also Nielsen et al., Science, 1991, 254, 1497-1500).
- 103. It is also possible to link other types of molecules (conjugates) to nucleotides or nucleotide analogs to enhance for example, cellular uptake. Conjugates can be chemically linked to the nucleotide or nucleotide analogs. Such conjugates include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Let., 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660, 306-309; Manoharan et al., Bioorg. Med. Chem. Let., 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J., 1991, 10, 1111-1118; Kabanov et al.,

FEBS Lett., 1990, 259, 327-330; Svinarchuk et al., Biochimie, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654; Shea et al., Nucl. Acids Res., 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14, 5 969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., J. Pharmacol. Exp. Ther., 1996, 277, 923-937. Numerous United States patents teach the preparation of such conjugates and include, but are not limited to U.S. 10 Pat. Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 15 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, each of which is herein incorporated by reference. 20

- 104. A Watson-Crick interaction is at least one interaction with the Watson-Crick face of a nucleotide, nucleotide analog, or nucleotide substitute. The Watson-Crick face of a nucleotide, nucleotide analog, or nucleotide substitute includes the C2, N1, and C6 positions of a purine based nucleotide, nucleotide analog, or nucleotide substitute and the C2, N3, C4 positions of a pyrimidine based nucleotide, nucleotide analog, or nucleotide substitute.
- 105. A Hoogsteen interaction is the interaction that takes place on the Hoogsteen face of a nucleotide or nucleotide analog, which is exposed in the major groove of duplex DNA. The Hoogsteen face includes the N7 position and reactive groups (NH2 or O) at the C6 position of purine nucleotides.

b) Sequences

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106. One particular sequence set forth in PTPN18 and having Genbank accession number NM 014369 is used herein, as an example, to exemplify the

disclosed compositions and methods. It is understood that the description related to this sequence is applicable to any sequence related to PTPN18 unless specifically indicated otherwise. Those of skill in the art understand how to resolve sequence discrepancies and differences and to adjust the compositions and methods relating to a particular sequence to other related sequences. Primers and/or probes can be designed for any PTPN18 sequence given the information disclosed herein and known in the art.

c) Primers and probes

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- 107. Disclosed are compositions including primers and probes, which are capable of interacting with the PTPN18 gene as disclosed herein. In certain embodiments the primers are used to support DNA amplification reactions. Typically the primers will be capable of being extended in a sequence specific manner. Extension of a primer in a sequence specific manner includes any methods wherein the sequence and/or composition of the nucleic acid molecule to which the primer is hybridized or otherwise associated directs or influences the composition or sequence of the product produced by the extension of the primer. Extension of the primer in a sequence specific manner therefore includes, but is not limited to, PCR, DNA sequencing, DNA extension, DNA polymerization, RNA transcription, or reverse transcription. Techniques and conditions that amplify the primer in a sequence specific manner are preferred. In certain embodiments the primers are used for the DNA amplification reactions, such as PCR or direct sequencing. It is understood that in certain embodiments the primers can also be extended using non-enzymatic techniques, where for example, the nucleotides or oligonucleotides used to extend the primer are modified such that they will chemically react to extend the primer in a sequence specific manner. Typically the disclosed primers hybridize with the PTPN18 gene or region of the PTPN18 gene or they hybridize with the complement of the PTPN18 gene or complement of a region of the PTPN18 gene.
- 108. The size of the primers or probes for interaction with the PTPN18 gene in certain embodiments can be any size that supports the desired enzymatic manipulation of the primer, such as DNA amplification or the simple hybridization of the probe or primer. A typical PTPN18 primer or probe would be at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79,

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80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1250, 1500, 1750, 2000, 2250, 2500, 2750, 3000, 3500, or 4000 nucleotides long.

- 109. In other embodiments an PTPN18 primer or probe can be less than or equal to 6, 7, 8, 9, 10, 11, 12 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1250, 1500, 1750, 2000, 2250, 2500, 2750, 3000, 3500, or 4000 nucleotides long.
- 110. The primers for the PTPN18 gene typically will be used to produce an amplified DNA product that contains a region of the PTPN18 gene. In general, typically the size of the product will be such that the size can be accurately determined to within 3, or 2 or 1 nucleotides.
 - 111. In certain embodiments this product is at least 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1250, 1500, 1750, 2000, 2250, 2500, 2750, 3000, 3500, or 4000 nucleotides long.
- 112. In other embodiments the product is less than or equal to 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1250, 1500, 1750, 2000, 2250, 2500, 2750, 3000, 3500, or 4000 nucleotides long.

4. Compositions identified by screening with disclosed compositions / combinatorial chemistry

a) Computer assisted drug design

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- 113. The disclosed compositions can be used as targets for any molecular modeling technique to identify either the structure of the disclosed compositions or to identify potential or actual molecules, such as small molecules, which interact in a desired way with the disclosed compositions. The nucleic acids, peptides, and related molecules disclosed herein can be used as targets in any molecular modeling program or approach.
- 114. It is understood that when using the disclosed compositions in modeling techniques, molecules, such as macromolecular molecules, will be identified that have particular desired properties such as inhibition or stimulation or the target molecule's function.
 - through rational design. This is achieved through structural information and computer modeling. Computer modeling technology allows visualization of the three-dimensional atomic structure of a selected molecule and the rational design of new compounds that will interact with the molecule. The three-dimensional construct typically depends on data from x-ray crystallographic analyses or NMR imaging of the selected molecule. The molecular dynamics require force field data. The computer graphics systems enable prediction of how a new compound will link to the target molecule and allow experimental manipulation of the structures of the compound and target molecule to perfect binding specificity. Prediction of what the molecule-compound interaction will be when small changes are made in one or both requires molecular mechanics software and computationally intensive computers, usually coupled with user-friendly, menu-driven interfaces between the molecular design program and the user.
 - 116. Examples of molecular modeling systems are the CHARMm and QUANTA programs, Polygen Corporation, Waltham, MA. CHARMm performs the energy minimization and molecular dynamics functions. QUANTA performs the construction, graphic modeling and analysis of molecular structure. QUANTA allows interactive construction, modification, visualization, and analysis of the behavior of molecules with each other.

with specific proteins, such as Rotivinen, et al., 1988 *Acta Pharmaceutica Fennica* 97, 159-166; Ripka, *New Scientist* 54-57 (June 16, 1988); McKinaly and Rossmann, 1989 *Annu. Rev. Pharmacol._Toxiciol.* 29, 111-122; Perry and Davies, <u>OSAR: Quantitative Structure-Activity Relationships in Drug Design</u> pp. 189-193 (Alan R. Liss, Inc. 1989); Lewis and Dean, 1989 *Proc. R. Soc. Lond.* 236, 125-140 and 141-162; and, with respect to a model enzyme for nucleic acid components, Askew, et al., 1989 *J. Am. Chem. Soc.* 111, 1082-1090. Other computer programs that screen and graphically depict chemicals are available from companies such as BioDesign, Inc., Pasadena, CA., Allelix, Inc, Mississauga, Ontario, Canada, and Hypercube, Inc., Cambridge, Ontario. Although these are primarily designed for application to drugs specific to particular proteins, they can be adapted to design of molecules specifically interacting with specific regions of DNA or RNA, once that region is identified.

118. Although described above with reference to design and generation of compounds which could alter binding, one could also screen libraries of known compounds, including natural products or synthetic chemicals, and biologically active materials, including proteins, for compounds which alter substrate binding or enzymatic activity.

5. Kits

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practicing the methods disclosed herein. The kits can include any reagent or combination of reagent discussed herein or that would be understood to be required or beneficial in the practice of the disclosed methods. For example, the kits could include primers to perform the amplification reactions discussed in certain embodiments of the methods, as well as the buffers and enzymes required to use the primers as intended. For example, disclosed is a kit for assessing a subject's risk for CFS, comprising a microarray with probes.

D. Methods of using the compositions

- 1. Methods of using the compositions as diagnostic and research tools
- 120. The disclosed compositions can be used in a variety of ways as research tools. For example, the disclosed compositions, can be used to study the interactions between genes associated with neuronal, endocrine, and immune responses.

121. The disclosed compositions can also be used diagnostic tools related to diseases, such as CFS, inflammatory conditions, cancer, infectious diseases including but not limited to viral, bacterial, fungal, and parasitic infections.

- 122. Throughout this application, various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains. The references disclosed are also individually and specifically incorporated by reference herein for the material contained in them that is discussed in the sentence in which the reference is relied upon.
- 123. It will be apparent to those skilled in the art that various modifications and variations can be made in the present invention without departing from the scope or spirit of the invention. Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

E. Examples

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skill in the art with a complete disclosure and description of how the compounds, compositions, articles, devices and/or methods claimed herein are made and evaluated, and are intended to be purely exemplary of the invention and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers (e.g., amounts, temperature, etc.), but some errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, temperature is in °C or is at ambient temperature, and pressure is at or near atmospheric.

1. Example 1

- a) Evaluation of a Psychoneuroendocrinimmune (PNI)
 Microarray as a tool for gene expression profiling of Chronic
 Fatigue Syndrome and other complex diseases resulting from
 dysregulation of the Hypothalamic-Pituitary-Adrenal axis
- 125. Due to the complexity of interactions between immune, endocrine, and nervous systems, assays for one or a few biomolecular markers can be uninformative or

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misleading. Accordingly, diseases which are characterized by disturbances in one or more of these systems, and the interactions between them, are among the most significant research and clinical challenges. An oligonucleotide microarray composed entirely of PNI genes (the PNI array) was designed, which can allow a researcher to assess the overall psychoneuroendocrineimmune state of an individual, and to observe systemic responses to various stressors. The PNI array has widespread applicability and marketability in the diagnosis and treatment of diseases that result from dysregualtion of the HPA axis. A total of 1451 genes encoding 1738 transcriptional products are represented on the PNI array, and gene choices were guided by the goal of elucidating biological pathways. Splice variants of the PNI genes can be distinguished, and samples from human or mouse can hybridize with equal affinity, facilitating animal studies. Described here is a series of discrete projects designed to validate results obtained using the PNI array, and demonstrate its utility for research of Chronic Fatigue Syndrome and other diseases involving PNI.

Microarray technology allows discovery of gene expression patterns, which can be more meaningful than observations about fluctuations in expression levels of individual genes. Peripheral blood has been shown to contain distinctive gene expression patterns in several diseases which cannot easily be studied. Vernon, et al. compared individuals with Chronic Fatigue Syndrome to healthy controls using gene expression profiling, and found evidence for nervous and immune system dysfunction in the CFS patients (Vernon, et al., 2002, which is hereby incorporated by reference in its entirety for it's teaching of use of a microarray to determine the expression profiles of patients with CFS and the expression profiles for CFS patients). Like many other diseases, CFS is caused or maintained by psychoneuroendocrineimmune (PNI) dysregulation, possibly due to HPA axis malfunction (Figure 1). Some of these other well-studied diseases are manifestly physical, including type-2 diabetes (Rosmond, 2003), allergic conditions including atopic dermatitis (Buske-Kirschbaum, et al., 2002), rheumatic diseases such as rheumatoid arthritis and systemic lupus erythematosus (Crofford, 2002; Wilder, 2002), coronary heart disease (Yudkin, et al., 2000), and inflammatory bowel disease (Straub, et al., 2002). Others, such as acute depression (Parker, et al., 2003), fatigue diseases resulting from defined causes, such as cancer treatment (Morrow, et al., 2002), or as yet undefined causes, including chronic fatigue syndrome (CFS) (Parker, et al., 2001; Racciatti, et al., 2001), post traumatic stress

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disease (Yehuda, 2001), susceptibility to alcoholism (Hernandez-Avila, et al., 2002), Alzheimer's Disease (Peskind, et al., 2001), and cognitive impairment resulting from multiple sclerosis (Heesen, et al., 2002; Then Bergh, et al., 1999), have a neurological component and result in a reduced sense of well-being.

127. Unfortunately, the microarray community is increasingly realizing that with recent advances in technology, the bottleneck has shifted from data production to data analysis. Sifting through the immense quantity of data produced by wholegenome arrays is a daunting task, particularly for researchers who are truly interested only in a subset of genes, representing one or a few functional systems.

128. In order to remedy this oversight, a novel oligonucleotide microarray was designed and produced for detection of changes in the signals being sent between the brain and nervous system and the immune and endocrine systems. A list of genes was compiled encoding proteins that participate in modulation of immune, neuroendocrine, endocrine, or nervous system functions. Particular emphasis was placed on identifying genes acting in the HPA axis.

Oligos were selected from the coding sequence of the PNI genes. In 129. addition to the standard considerations for oligo selection, two additional criteria were applied. Firstly, oligos were chosen that will allow very precise determination of relative abundance of each transcriptional variant. This can be important, as transcriptional variants can possess differing, even self-negating, functions. For example, the ZER6 transcription factor has two isoforms, only one of which interacts with estrogen-receptor alpha, and the relative level of expression of these two isoforms regulates transcription by hormone-responsive cells (Conroy, et al., 2002). Alterations in ratios between transcriptional variants can be characteristic of disease state, as is the case with certain transcripts of BDNF (Brain Derived Neurotropic Factor) in Alzheimer's disease patients (Garzon, et al., 2002). Transcriptional variants of the FGF-inducible mi-er1 gene differ in their subcellular localization (Paterno, et al., 2002), and several proteins are produced in both soluble and membrane-bound isoforms (Kapur, et al., 2002; Tenhunen & Ulmanen, 1993). Secondly, the selected oligos match nucleotide sequences that are either identical in both human and mouse gene homologs, or contain only a few mismatches on the 5' end. Consequently, the PNI array can be useful for researchers using mouse as a model system for human disease, and results from human and mouse studies using the PNI array are directly comparable.

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130. Each gene was annotated in a customized Microsoft Access database to include functional information, alternate gene names, and protein, mRNA, and coding sequences. 1451 non-redundant genes were included, several of which encoded multiple transcriptional products representing functional regulation at the RNA level. The entries were standardized to the NCBI RefSeq project, to facilitate future analyses. Figure 2 shows the composition of this array.

- 131. Nimblegen has two design formats available, 196K and 85K. Ten slides were received from Nimblegen in the 196K format. The standard hybridization protocol was found to produce a good dynamic range of signal intensity on these slides, with minimal background (Figure 3a). However, it was clear that the extremely small size of these spots complicated data extraction. A sample 85K data file received from Nimblegen revealed that the 85K format allows reliable data retrieval (Figure 3b).
- 132. While the uses for a microarray of this design in basic research are immediately apparent, the real interest is in its utility for clinical application. Because the peripheral blood is a rich source of immune cells, and a readily available tissue sample, the utility of a PNI microarray in analysis of blood samples was evaluated.
- 133. This sort of analysis is unfortunately confounded by the fact that most neurotransmitters and hormones are produced, and act, at sites distinct from the peripheral blood. Additionally, the microenvironment of the brain is protected by the blood-brain barrier, a lipid membrane that under normal conditions excludes cells, both bacterial and immune, as well as most large molecules (Paulson, 2002). There are several mechanisms by which dysregulation of PNI interactions can be reflected in peripheral blood gene expression patterns. One is changes in cytokine production would be detected, as would changes in expression levels of genes that are regulated by circulating hormones, neurotransmitters, and growth factors. Another is inappropriate neuroendocrine gene expression in circulating immune cells. Inflammatory cytokine release, excessive stress, or other as yet unidentified PNI disturbance may increase permeability of the blood-brain barrier to leukocyte infiltration, exposing these cells to the microenvironment of the brain and changing their gene expression patterns. Lastly, peripheral blood can play a more active role in producing appropriate PNI response than has previously been suspected.
- 134. In order to bioinformatically simulate microarray analysis of PNI genes in peripheral blood, an Expressed Sequence Tag (EST) database was compiled from

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NCBI's dbEST using nine EST libraries prepared using normal human blood samples. Libraries prepared from tumor cell lines or leukemia samples were excluded from the analysis due to concerns that pathological alterations in gene expression of these cells would be a confounding factor. The ESTs were formatted into a blastable database of approximately 30,000 sequences. Of the 1451 genes, 505 were detectable in the blood EST database. The majority were previously characterized as expressed in blood, with some interesting exceptions. The preferential expression of immune system genes in peripheral blood cells (52% of the detected genes were in the immune system category, as compared to 40% of all PNI genes examined) was expected, but evidence of peripheral blood expression of many genes involved in endocrine and neuronal processes was exciting and informative.

- apoptosis than whole blood, as measured by Annexin V binding. Additional studies showed considerable change in gene expression subsequent to collection by standard methods, as compared to the PAXgene whole blood collection system supplied by Qiagen (figure 4). It is certainly possible that previous studies of chronic fatigue syndrome that relied on data collected from isolated PBMCs were confounded by this phenomenon, and the present PNI array is well suited for investigating this possibility.
- 136. PBMCs can be obtained from whole blood collected in the presence of EDTA. Whole blood can be collected in parallel using the Qiagen PAXgene blood RNA system. RNA can be extracted from each sample using Trizol, and quantified by a RiboGreen assay. RNA samples can be reverse-transcribed in the presence of biotin-11-UTP, then hybridized to the oligonucleotides on glass array slides using the Ventana Automated Hybridization instrument. The biotinylated sample hybridized to the oligonucleotides can be detected at 600nm using RLS-gold particles. Signal intensity data can be collected with Arrayvision software.
- 137. Next, the possibility that isolation of PBMCs changes the gene expression profiles of the cells is addressed by comparing RNA extracted from whole blood by the two different collection methods, both to each other and to results of analysis of PBMCs. Based on these results a preferred method of blood handling can be selected. From three individuals, three alliquots of blood can be collected. One alliquot can be collected using the Qiagen PAXgene system, and the second and third aliquots can be collected using standard methods. One of these can be processed to

isolate PBMCs. RNA is extracted as soon as possible after blood is collected from the first individual, and after delays of four and twenty-four hours after blood is collected from the second and third individuals, respectively.

- 138. Finally, results obtained from the PNI array can be directly compared to results from MWG 30K arrays (MWG Biotech Inc.'s 30K array). Blood samples are collected from two individuals using the selected method, and divided into two aliquots. One aliquot from each sample can be hybridized to each of the two arrays. The subset of oligos on the MWG 30K array that correspond to one of the genes on the PNI array can be selected for comparison.
- 139. Monozygotic (MZ) twins are presumed to share 100% of their genes and to have been raised in similar environments (with the exception of twins separated at birth). As a result, twin studies are a classic method for examining heritability of incompletely penetrant genetic traits. Comparisons of gene expression profiles of monozygotic twins can be particularly informative, as the heritable individual variability in expression of a wide range of genes that confounds many microarray studies would be quantifiable within this population. As a result, consistent differences in gene expression profiles of MZ twins disconcordant for CFS are more readily distinguished.

2. Example 2

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pituitary-adrenal (HPA) axis. It would therefore be of great value to be able to characterize changes in peripheral blood gene expression patterns that are reflective of HPA axis dysregulation. The HPA axis is a homeostatic feedback loop, in which the hypothalamus secretes corticotropin releasing factor (CRF), which stimulates the pituitary to secrete adrenocorticotropic hormone (ACTH), which in turn directs the adrenals to secrete corticosteroids, providing negative feedback to the hypothalamus and pituitary (Figure 1). Each component of the HPA axis is regulated by a variety of external and internal stimuli, some of which are listed in Table 1 and Figure 6.

Table 1: A variety of factors up-regulate (+) or down-regulate (-) hypothalamus-pituitary-adrenal (HPA) axis activity

HPA axis component	Regulating factors
Hypothalamus (PVN or	Cytokines and Growth Factors (+/-)
paraventricular nucleus)	Neural Inputs (+/-)
	Sex Hormones (+/-)
1	Prostaglandins (+)
	Leptin (+/-)
	Neuropeptides (+/-)
Pituatary (corticotrope)	Cytokines and Growth Factors (+/-)
	Vasopressin (-)
	Prostaglandins (-)
	Opiates (-)
	Catecholamines (+)
Adrenal	Cytokines and Growth Factors (+/-)
(fdrenal fasiculata)	Prostaglandins (+)
,	Sex Hormones (+/-)
	Neural Input (+/-)

- HPA axis dysfunction has been implicated in a variety of complex 141. diseases. Some of these are manifestly physical, including type -2 diabetes (Rosmond, 5 2003); allergic conditions including atopic dermatitis (Buske-Kirschbaum, et al., 2002); rheumatic diseases such as rheumatoid arthritis and systemic lupus erythematosus (Crofford, 2002; Wilder, 2002); Sjogren's syndrome (Johnson, et al., 2000); coronary heart disease (Yudkin, et al., 2000); and inflammatory bowel disease (Straub, et al., 2002). Others, such as acute depression (Parker, et al., 2003); fatigue diseases resulting 10 from defined causes, such as cancer treatment (Morrow, et al., 2002), or as yet undefined causes, including chronic fatigue syndrome (CFS) (Parker, et al., 2001; Racciatti, et al., 2001); post-traumatic stress disorder (Yehuda, 2001); susceptibility to alcoholism (Hernandez-Avila, et al., 2002); Alzheimer's Disease (Peskind, et al., 2001); and cognitive impairment resulting from multiple sclerosis (Heesen, et al., 15 2002; Then Bergh, et al., 1999), have a neurological component and result in a reduced sense of well-being.
 - breached when the PNI interactions are disrupted. Acute stress increases permeability of the blood-brain barrier due to release of CRF (Esposito, et al., 2003; Esposito, et al., 2002; Esposito, et al., 2001). Likewise, the limited ability of leukocytes and certain bacteria and viruses to penetrate between the endothelial cells into the brain is greatly enhanced by increased endothelial production of inter-cellular adhesion molecule-1

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(ICAM-1) (Dietrich, 2002). Because ICAM-1 expression is up-regulated by cytokines such as Tumor Necrosis Factor-α (Wong & Dorovini-Zis, 1992) and down-regulated by glucocorticoid hormones (Liden, et al., 2000) and interferon-β (Floris, et al., 2002), immunological disturbances can alter the permeability of the blood-brain barrier. This is not merely a theoretical possibility: compelling evidence has linked this increased permeability to central nervous system disorders such as multiple sclerosis (Greenwood, et al., 2002). Even when the blood-brain barrier remains intact, the brain can be affected by changes in expression of PNI genes. As an example, increased serum levels of insulin-like growth factor-1 promote the clearance of amyloid-β from the cortex and hypothalamus (Carro, et al., 2002).

- 143. Thus, there are several mechanisms by which dysregulation of PNI interactions could be reflected in peripheral blood gene expression patterns. The most likely to be detected are changes in cytokine production and changes in expression levels of genes that are regulated by circulating hormones, neurotransmitters, and growth factors. Inappropriate neuroendocrine gene expression in circulating immune cells would be detected, but is unlikely. Also possible is a more active role than has previously been suspected for peripheral blood in producing an appropriate PNI response. Lastly, inflammatory cytokine release, excessive stress, or other as yet unidentified PNI disturbances that increase permeability of the blood-brain barrier to leukocyte infiltration, exposing them to the microenvironment of the brain and producing gene expression alterations that can remain detectable upon re-entry to the blood stream.
- patterns in gene expression. This is significant, as these patterns provide the context for specific observations. For certain complex diseases, distinctive peripheral blood gene expression patterns have been characterized. In one example, individuals with chronic fatigue syndrome (CFS) were compared with healthy controls by gene expression profiling, and evidence for altered expression of immune and nervous system genes in the CFS patients was found (Vernon, et al., 2002).

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a) Methods & Materials

145. A list of genes encoding proteins that participate in modulation of immune, neuroendocrine, endocrine, or nervous system functions was compiled.

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Particular emphasis was placed on functions mediated by the HPA axis. Each gene was annotated in a customized Microsoft Access database to include functional information, alternate gene names, and both protein and mRNA sequences. One thousand four hundred fifty one non-redundant genes were included, several of which encoded multiple transcriptional products representing functional regulation at the RNA level. The entries were standardized to the National Center for Biotechnology Information (NCBI) RefSeq project, to facilitate future analyses.

- 146. To determine expression of these candidate genes in circulating blood, an expressed sequence tag (EST) database was compiled from NCBI's GenBand EST database (dbEST) using nine EST libraries prepared using normal human blood samples. Libraries prepared from tumor cell lines or leukemia samples were excluded because the pathological alterations in gene expression of these cells were considered likely to confound the analysis. The ESTs were formatted into a blastable database of approximately 30,000 sequences, each of which could be directly traced to its original dbEST entry and was by definition representative of gene expression detectable in blood samples.
- 147. The 1451 PNI genes represent hormones, neurotransmitters, and cytokines, which are the principal signaling molecules of the endocrine, neuronal, and immune systems respectively, and a variety of genes whose expression or activities are regulated by these signals. Table 2 categorizes the PNI genes according to predominant system and subcategorizes them by function. The largest group of genes selected, representing slightly more than 40%, were the immune system genes, followed by endocrine (24%) and neuronal (14%) genes (Figure 5A). The remaining genes either have well characterized roles in multiple systems, or were of interest primarily due to their functional or regulatory characteristics, and thus were designated as "other". Of the 1451 genes, 505 were detectable in the blood EST database (Figure 5B).
- 148. Most of PNI genes identified in the database were previously characterized as expressed in blood, with some interesting exceptions. The preferential expression of immune system genes in peripheral blood cells (52% of the detected genes were in the immune system category, compared to 40% of all PNI genes examined) was expected, but peripheral blood expression of many genes involved in endocrine and neuronal processes was quite intriguing.

Table 2: Details of the categorical distribution of PNI genes.

		Found In	
Category	PNI genes	Blood	(%)
Endocrine System			
Hormone Metabolism	79	17	(22)
Hormone Receptor	95	12	(13)
Hormones	45	[,] 1	(2)
Regulated by Hormones	28	11	(39)
Regulates Hormone Activity	53	25	(47)
Regulates Hormone Expression	18	6	(33)
Other Neuroendocrine Function	30	12	(40)
Nervous System			
Neurotransmitter	20	0	. (0)
Neurotransmitter Metabolism	32	10	(31)
Neurotransmitter Receptor	100	3	(3)
Regulated by Neurotransmitters	2	1	(50)
Regulates Neurotransmitter Activity	v 51	10	(20)
Regulates Neurotransmitter			, ,
Expression	1	0	(0)
Immune System			, ,
Apoptosis	40	26	(65)
Complement Component	29	7	(24)
Cytokine or Chemokine Receptors		38	(42)
Cytokines and Chemokines	108	31	(29)
MHC/HLA	18	17	(94)
Regulated by Cytokines or			` ,
chemokines	9	4	(44)
Regulates Cytokine Activity	20	7	(35)
T-cell Activation	6	3	(50)
Other Immune Function	261	134	(51)
Signal Transduction	55	31	(56)
Protease Inhibitor	9	4	(44)
Transcription Factor	92	44	(48)
Circadian	7	4	(57)
Regulation of Cell Growth	40	6	(15)
Growth Factor	26	5	(19)
Growth Factor Receptor	11	1	(9)
Heat shock	20	11	(55)
	10	9	(90)
Stress Response		5	(16)
Homeostasis & Small Molecule transport	10	7	(70)
Other	4	3	(75)
Unknown Function	1451	<u>5</u>	(35%)
Total (Non-redundant)	1401	300	(00/0)

b) Results & Conclusion

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- 149. Bioinformatic evidence suggests that circulating blood cells can respond to hormones and neurotransmitters. As would be expected, there is no evidence for production of hormones or neurotransmitters in the peripheral blood, with the interesting exception of the putative hormone ADM. This hypotensive peptide, which can have neurotransmitter activity, is known to be present in both blood and the central nervous system (Serrano, et al., 2002). However, there was evidence for expression of both neurotransmitter and hormone receptors.
- 150. Table 3, which is provided herein on compact disc and is incorporated herein in its entirety, shows the gene names, accession numbers, and the human and corresponding mouse sequences for each of the genes on the PNI array. Table 3, created on June 4, 2004 containing 4,608 KB of information, is provided conforming to ISO 9660 standards as a MS Windows XP compatible MS EXCEL XP ASCII file on each of 3 discs.
- EST sequences representing both the GABA(B) receptor and GABARAP 151. (γ-aminobutyric acid type A receptor-associated protein) were identified, implying the existence of a systemic (GABA)ergic response. Participation of the (GABA)ergic system in immunomodulation has long been recognized (Devoino, et al., 1992), and the role of GABA(A) receptors in stimulating release of hypothalamic and pituitary hormones in response to cytokine activity has been well described (McCann, et al., 2000). A more direct role was indicated by the discovery of a functional GABA(A) receptor on the surface of T cells (Tian, et al., 1999). It is the GABA_{B(1e)} splice variant, which is secreted and competes with GABA_{B(1a)} for dimerization with GABA_{B(2)} (Schwarz, et al., 2000), that is described in peripheral blood and which is perhaps secreted by immune cells to directly regulate the (GABA)ergic system. Peripheral blood expression of the ADRB2 protein, a norepinephine receptor that has a well-documented role in regulating immunity (Sanders & Straub, 2002), and the acetylcholine receptor CHRNB1, which was previously identified as expressed on T and B cells (Hiemke, et al., 1996; Toyabe, et al., 1997) was confirmed.
- 152. Of the hormone receptors found in peripheral blood, the surprising presence of membrane-associated progesterone receptor PGRMC1 is particularly interesting. The rat homolog has been shown by differential display PCR to be expressed in the hypothalamus and to regulate female reproductive behavior (Krebs, et

al., 2000). The presence in peripheral blood of a hormone receptor that is also expressed in brain and has a known behavioral function is unexpected.

- 153. Other proteins were of interest due to their capacity to be induced by hormonal activity. One of these was ZNF147, also known as Efp (estrogen-responsive finger protein), which is up-regulated by estrogen and down-regulated by transforming growth factor-β (Inoue, et al., 1993; Inoue, et al., 1999). ZNF147 acts by targeting the 14-3-3sigma protein for proteolysis (Urano, et al., 2002). Since 14-3-3sigma sequesters Bax (Samuel, et al., 2001), which plays an essential role in T-cell development (Bouillet & Strasser, 2002), the presence of this protein in peripheral blood can represent a direct mechanism for endocrine influence on immune function.
- 154. Examining peripheral blood samples for gene expression patterns representative of PNI dysfunction presents certain challenges, but this analysis shows here how informative it can be. By using peripheral blood to "profile the brain" and characterize the PNI response, insights can be gained about many complex diseases in which there is thought to be PNI dysregulation. This approach can be especially important for diseases for which there is no known lesion, or when known lesions cannot be sampled. Furthermore, this survey of peripheral blood gene expression in relation to PNI function provides evidence to interactions between the endocrine, immune, and nervous systems which had not been previously expected.

3. Example 3

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- 155. Chronic fatigue syndrome appears to be either caused or sustained by dysregulation of the neuroendocrine and/or immune systems. CFS has been shown to be refractory to the established methods of treating circadian disorders, including melatonin thearpy.
- performed by measuring the levels of relevant proteins or hormones in circulating blood or other bodily fluids. This approach has been productive for studies which focus on a limited number of molecules, but it is less useful for analysis of systemic changes involving multiple signaling pathways. An experimental approach that is much more amenable to analysis of systemic changes is gene expression profiling. The limitation to gene expression profiling of neuroendocrine genes is that the available sample, blood, is not the normal site of expression for many of these genes. However, these results indicate that despite this limitation, assessing the immune and

neuroendocrine irregularities of CFS patients by gene expression profiling of blood samples can be very informative. Herein is described the production of oligonucleotide microarrays, designed to measure expression of genes which encode proteins involved in neuroendocrine/immune interactions, and intended to provide specific information about the expression of known and novel genes in blood.

4. Example 4

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a) Background

157. The first iteration of the PNI array is derived from a PNI gene list of 1622 genes. 1435 of the genes encode a single known transcriptional variant, while the remainder encode multiple splice variants, so a total of 1958 transcriptional products are represented. For the majority of the transcriptional products, both human and mouse sequences were either retrieved from the public databases (i.e. Genbank), or could be deduced from publicly available genomic sequences.

b) Probe Selection

- 158. This first iteration of the PNI array is composed entirely of genes which encode at least one 24-mer that is common to both human and mouse homologs of the gene, with the exception of Arabidopsis controls. In addition, probes were screened to eliminate long (>4) runs of any single nucleotide, or extremes of melting temperature. (Depending on which equation is used, probes fall in a Tm range of approx 50-85°F, or 60-95°F. This is a much greater temperature range than is ultimately desirable for microarray analysis, but a reasonable range for selecting probes to be tested empirically).
- at least one 24-mer meeting the above described criteria. These are designated as NoSplice probes. An additional 18 housekeeping genes with a single known splice variant yielded probes meeting the criteria, and probes representing these genes were designated Housekeeping probes. Mismatched probes can be made to the probes from two of these genes (1, 2, 3, and 4 mismatches) for use as a stringency control. A second type of control probe, designed to hybridize to one of ten Arabidopsis genes (for which mRNA is commercially available), was included. Fifty 24-mers meeting the above criteria were selected at random for each gene. Probes encoding the Arabidopsis gene LTP4 can be biotinylated, serving as a positive control for the signal detection process.

analysis, and can be much more sensitive in detecting alterations in transcriptional abundance than traditional methods. Variants containing unique exons can be detected by probes specific to those exons. Variants lacking unique exons can be detected by two methods: probes complementary to unique splice junctions, and by comparison of the signal intensity of probes which detect exons shared with other variants, in conjunction with information about the expression of those variants. Conditions for these probes have been optimized (Optimization of oligonucleotide arrays and RNA amplification protocols for analysis of transcript structure and alternative splicing; Genome Biology 2003, 4:R66). Huge strides forward have been made in collecting and annotating splice variant information for human (Kan Z, et al. (2001) Genome Res 11, 889-900, Thanaraj, T. (1999) Nucleic Acids Res 27, 2627-37, Christopher Lee, et al (2003) Nucleic Acids Research 31, 101-105) and mouse (Kochiwa H, et al. (2002) Genome Res 12, 1286-93) genomes.

- 161. Algorithms exist for detection of novel transcriptional variants (Hu GK, et al. (2001) Genome Res 11, 1237-45, hereby incorporated by reference in it's entirety for the disclosure of algorithms) and for validation of predicted variants (D. D. Shoemaker, et al. (2001) Nature 409, 922 927, hereby incorporated by reference in it's entirety for the disclosure of algorithms). However, often a biologist in the process of designing a custom microarray is confronted with the situation where many or all of the transcriptional variants of the genes of interest are known, and probes capable of differentiating these variants are desired. Typically, the known variants would be entered into a multiple alignment program, and candidate probes selected based on the results of this alignment. However, this process of manual probe selection is labor intensive, and rather tedious to repeat the hundreds or thousands of times that would be necessary for custom microarray development.
- 162. The SpliceVariants macro takes an iterative approach to probe selection. For each gene in sequence, it detects the gene abbreviation then counts the number of variants, collecting the variant's unique abbreviation in the process into a multi-dimensional array. Once it reaches the end of the file, or encounters a gene abbreviation for a different gene, it returns to the first variant and counts the number of nucleotides. It then begins the process of probe selection. The researcher specifies the length of the oligo desired, and every possible n-mer of that length is analyzed.

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variants contain that n-mer. The n-mer is placed into an array of probes that are unique, shared, or common to all variants, as appropriate, and its positions noted. The program then moves over one nucleotide, and repeats the process, iteratively, until the number of variants containing a given n-mer differs from the first in the series. This occurs at an alternatively spliced exon boundary. It is entirely possible that several exons can be shared consecutively by a group of variants, but the position of these exon boundaries is unimportant for the task at hand, so only exon boundaries where alternative splicing occurs are considered. In the interest of brevity, the word "exon" shall be used to refer also to groups of exons which are consecutive in this manner.

- 164. Once a junction between alternately spliced exons is detected, a set of candidate junction probes is generated for each appropriate variant. The length of the exon is saved along with the sequence of the first n-mer from that exon. This process repeats until the end of the first variant is reached.
- 165. The second, and subsequent, variants can contain one or more exons in common with previous variants. The computational time required is significantly reduced by comparing the first n-mer of each new exon encountered with the first n-mer of all previous exons. If they are identical, it is assumed that the remaining n-mers for the exon are similarly identical, and the program skips ahead to the beginning of the next exon.
- 166. After all variants for a given gene have been considered, the program goes to the beginning of the page and outputs the sequences of the unique, common, shared, and junction probes which have been detected. For each probe, a non-redundant probe name is generated which contains information regarding the type of probe (ie unique or common) and the variant or variants in which it occurs. If there is another gene to be analyzed, it repeats.
- 167. By approaching this challenge as a word-processing problem, a de facto multiple alignment of transcriptional variants was accomplished without actually requiring the use of a multiple alignment algorithm. The resulting lists of candidate probes corresponding to unique, shared, or common exons can be used for production of any custom microarray that distinguishes transcriptional variants.
- 168. The remaining PNI genes are represented by multiple transcriptional variants. A number of these genes were entered into the algorithm written for selection

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of probes distinguishing transcriptional variants, but the majority were not due to time constraints. This algorithm yielded probes which were either Common to all variants (designated probe types are indicated by capitalization), Unique to a single variant, Shared between several but not all variants, or present at a splice Junction and capable of distinguishing variants with differing junctions. All PNI genes with multiple splice variants were independently entered into the algorithm written for selection of probes identical in both human and mouse homologs, and redundancies in this list were eliminated. The lists of probes were compared, and probes appearing on both lists were selected for further analysis. Probes derived from sequences of multi-variant genes which have not yet been entered into the SpliceVariants algorithm are designated as MultiVar probes.

- 169. Many of the genes are represented by large numbers of probes. In those cases where there were fewer than 100 probes meeting the above criteria, all eligible probes were selected for subsequent analysis. In cases where greater than 100 probes met the criteria, 50 were chosen at random for subsequent analysis.
- secondary structures, and uniqueness within the human genome. Balancing the results of these evaluations with the need to retain at least one probe for each of the genes of interest (although nine housekeeping genes were eliminated as no high-quality probes could be generated from their sequences), a final list of 12450 probes was generated. The distribution of probe types is given in Table 4, and the names of the genes/gene variants and number of probes generated from each sequence is shown in Table 5. A total of 1132 PNI genes are represented in this first iteration of the PNI array, along with 19 genes included as housekeeping or Arabidopsis controls.

Table 4	

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	Number
Probe Type	of probes
Arabidopsis	132
Arabidopsis-Biotinylated	16
Common	286
Housekeeping	159
Housekeeping Mismatch	60
Junction	9
MultiVar	1294
NoSplice	10355
Shared	20
Unique	119
Total	12450

c) Second iteration PNI array

- 171. As the understanding of immune, neurological, and endocrine processes increases, important roles for a larger number of specific proteins in these processes are being learned. Thus, the second iteration of the PNI array can be generated from a larger initial gene list. The second iteration of the PNI array can be generated from an initial gene list containing 2000-3000 genes, representing 5000-6000 transcriptional products.
- between human and mouse sequences are still important, and the second iteration of the PNI array can contain 24-mers from regions substantially different between the human and mouse homologs (one for human, one for mouse) so that the array can be a tool useful for animal model studies as well as human clinical studies. These probes lack the advantage that the perfectly conserved probes have, of allowing direct comparison between human and mouse samples, but they can be necessary for complete coverage of psycho-neuroendocrine-immune gene expression.
- 173. The first iteration of the PNI array has relatively few probes designed to differentiate between transcriptional variants, yet the functional differences between these variants make it important that they be distinguished on the second iteration. Lastly, the average number of probes per gene can be reduced on the second iteration, by selecting empirically determined optimal probes using the first iteration PNI array.
- 174. The Nimblegen 1st iteration PNI array has three adjacent replicates of the PNI array, and that the configuration of probes is randomized in each, but that the

location of each probe can be identified unambiguously. As shown in figures 16 and 17, for a given probe sequence, there is some inter-slide variability. However, the reproducibility was quite good. For the 12259 PNI probes where at least one of the three replicates had a sARMdens/background ratio of 2.5 or greater, the maximum and minimum log2sARM signal intensity was calculated, and the max/min ratio was calculated. The mean ratio was 1.27, and 95% of all max/min ratios fell between 1.21 and 1.33. There was only a slight position effect between the three replicate arrays, and signal intensities were distributed similarly overall.

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Table 5		
Probe Type	Gene or Variant	Number of probes
NoSplice	Α	7
NoSplice	A2M	1
NoSplice	AANAT	6
NoSplice	ABAT	10
NoSplice	ABCB1	42
Common	ACHE	15
Unique	ACHE vE4-E6	5
Housekeeping Mismatch	ACTB	16
Housekeeping	ACTB	4
NoSplice	ADA	4
NoSplice	ADCYAP1	12
NoSplice	ADCYAP1R1	15
NoSplice	ADRA2A	7
NoSplice	ADRBK1	3
NoSplice	ADRBK2	13
NoSplice	AGRP	3
NoSplice	AHR	12
Common	AIF1	3
Unique	AIF1 v3	9
NoSplice	AIG-1	13
NoSplice	AIP	40
NoSplice	AKR1C3	5
NoSplice	AKT1	26
NoSplice	ALDH1A1	28
NoSplice	ALDH1A2	. 12
NoSplice	ALDH1A3	5
NoSplice	ALDH1B1	6
NoSplice	ALDH2	32
NoSplice	ALDH3A1	1
NoSplice	ALDH3A2	23
Common	ALDH5A1	2
NoSplice	ALDH6A1	19
NoSplice	ALDH7A1	4
NoSplice	ALDH9A1	8
NoSplice	ALOX12B	20
	£ 1	

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NoSplice	ALOX15B		7
NoSplice	ALOX5		8
NoSplice	ALOX5AP		٠ 7
NoSplice	ALOXE3	•	8
NoSplice	AMH		7
NoSplice	AMHR2		5
NoSplice	ANXA1		6
NoSplice	ANXA11		10
NoSplice	ANXA13		26
NoSplice	ANXA2		7
NoSplice	ANXA3		18
NoSplice	ANXA4		16
NoSplice	ANXA5		21
Common	ANXA6		9
NoSplice	ANXA8		47
NoSplice	APBA1		5
NoSplice	APBA2		40
NoSplice	APBA3		4
NoSplice	APLP1		8
NoSplice	APOE		2
NoSplice	APP -		9
NoSplice	AR		5
NoSplice	ARIX		24
NoSplice	ARNTL		6
Common	ARRB1		19
NoSplice	ASCL1		9
NoSplice	ASIP		18
NoSplice	ATF2		11
NoSplice	AVPR1A		8
NoSplice	AVPR1B		7
NoSplice	AVPR2		9
NoSplice	B2M		1
NoSplice	B7-H3		5
Common	BACE		14
Common	BACE2		3
NoSplice	BAT1		1
NoSplice	BATF		3
Shared	BAX		1
NoSplice	BBOX1		7
Common	BCL2		6
NoSplice	BCL2A1		5
Common	BCL2L1		3
Unique	BCL2L1 v1		15
NoSplice	BCL2L2		16
NoSplice	BDKRB1		25
NoSplice	BDKRB2		8
NoSplice	BDNF		18
NoSplice	BF		3
Common	BLR1		2
NoSplice	BMX		7
NoSplice	BRE		11

NoSplice	E	BRS3				4
NoSplice	E	3TK				12
NoSplice	(C1QBP				13
NoSplice	(C1R				4
NoSplice	(C1S				3
NoSplice		C2				3
NoSplice		C3				5
NoSplice	*	C4B				6
NoSplice	(C4BPA				2
NoSplice		C5				7
NoSplice		C5R1				3
NoSplice		C6				37
NoSplice		C7				7
NoSplice		C8A				6
NoSplice		C8B				20
NoSplice		C9				5
Arabidopsis		CAB				16
NoSplice		CACNA1B				5
NoSplice		CACNA1D				12
NoSplice		CACNB1				9
NoSplice		CACNB2				7
NoSplice		CACNB3				4
NoSplice		CACNB4				3
NoSplice		CACNG2				12
NoSplice		CADPS				4
NoSplice		CALCA				1
NoSplice		CALCB				2
NoSplice		CALCRL	•			26
NoSplice		CALCYON				8
NoSplice		CALR				11
NoSplice		CAMLG				12
NoSplice		CANX				3
NoSplice		CARD10				4
NoSplice		CARP				18
Common		CASP2				9
Common		CASP3				6
Common		CASP6				2
Common		CASP9				2
Unique		CASP9 vA				9
NoSplice		CCKAR				11
NoSplice		CCKBR				1
NoSplice		CCL19				4
NoSplice		CCL21				1
NoSplice		CCL5				9
Common		CCR2				5
NoSplice		CCR4				2
NoSplice		CCR5				8
NoSplice		CCR7				10
NoSplice		CCR8				1
NoSplice		CCRL1				3
NoSplice		CD19				10
-				50		

NoSplice NoSplice NoSplice	CD3E CD3G CD3Z		12 5 5
NoSplice	CD4		17
NoSplice	CD44		3
NoSplice	CD81		9
NoSplice	CD84		9
NoSplice	CDC37		2
NoSplice	CDKN1C		18
NoSplice	CDR2		9
NoSplice	CDV-1		3
NoSplice	CDX1		1
NoSplice	CEBPA		6
NoSplice	CEBPB		5
NoSplice	CEBPG		7
Housekeeping	CFL1		43
NoSplice	CFTR		8
NoSplice	CGA		3
Common	CHAT		17
NoSplice	CHRM1		3
NoSplice	CHRM2		15
NoSplice	CHRM3		8
NoSplice	CHRM4		3
NoSplice	CHRM5		22
NoSplice	CHRNA1	1	3
NoSplice	CHRNA10		15
NoSplice	CHRNA2		5
NoSplice	CHRNA3		36
NoSplice	CHRNA4		3
NoSplice	CHRNA5		7
NoSplice	CHRNA6		3
NoSplice	CHRNA7		11
NoSplice	CHRNA9		3
NoSplice	CHRNB1		5
NoSplice	CHRNB2		37
NoSplice	CHRNB3		13
NoSplice	CHRNB4		3 42
NoSplice	CHRND		9
NoSplice	CHRNE		59 59
NoSplice	CHRNG		15
NoSplice	CHUK		4
NoSplice	CIAS1		4
NoSplice	CISH CLC		7
NoSplice			13
NoSplice	CLOCK		3
NoSplice	CLU CMKI P1		10
NoSplice	CMKLR1 CML66		9
NoSplice	CNIH		7
NoSplice NoSplice	CNOT2		14
· · · · · · · · · · · · · · · · · · ·	CNO12 CNR2		6
NoSplice	CIVILE		•

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NoSplice	CNTF		24
NoSplice	CNTFR		5
NoSplice	COASTER		13
NoSplice	CPE		5
NoSplice	CPT1C		32
NoSplice	CPT2		11
NoSplice	CR2		2
NoSplice	CREBBP		10
NoSplice	CRHR1		3
NoSplice	CRHR2		9
NoSplice	CRL3		7
NoSplice	CROT		7
NoSplice	CRP		7
NoSplice	CRYAB		4
NoSplice	CSF1		6
NoSplice	CSF1R		4
NoSplice	CSF2RB		11
NoSplice	CSNK1E		4
NoSplice	CST		3
NoSplice	CST7		5
NoSplice	CTLA4		5
NoSplice	CTSD		1
NoSplice	CTSW		24
NoSplice	CX3CR1		20 20
NoSplice	CXCL12		2 0
NoSplice	CXCL14		11
NoSplice	CXCL3		21
NoSplice	CXCL9		1
NoSplice	CXCR3		3
NoSplice	CXCR4		5
NoSplice	CXCR6		4
NoSplice	CYP11A		5
NoSplice	CYP1A1		4
NoSplice	CYP1A2		3
NoSplice	CYP1B1		8
NoSplice	CYP21A2		6
NoSplice	CYP24		9
NoSplice	CYP27A1		8
NoSplice	CYP27B1		3
Common	CYP2A7		5
NoSplice	CYP2B6		2
NoSplice	CYP2C18		9
NoSplice	CYP2C9		18
NoSplice	CYP2D6		1
NoSplice	CYP2E1		6
NoSplice	CYP2J2		21
NoSplice	CYP39A1		5
NoSplice	CYP46		17
NoSplice	CYP4A11		8
NoSplice	CYP4B1		53
NoSplice	CYP4F11		7
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NoSplice	CYP4F2		6
NoSplice	CYP51		25
NoSplice	CYP7A1		9
NoSplice	CYP7B1		5
NoSplice	CYP8B1		5
NoSplice	CYSLTR1		11
NoSplice .	CYSLTR2		12
NoSplice	CYT19		5
NoSplice	DAP		5
NoSplice	DAPK1		5
NoSplice	DAT1		6
NoSplice	DBH		15
NoSplice	DBP		5
NoSplice	DDC		16
NoSplice	DIO2		19
NoSplice	DIO3		4
NoSplice	DLG3		9
NoSplice	DLK1		7
NoSplice	DMGDH		11
NoSplice	DPP4		9
Common	DPP8		14
NoSplice	DRD1		15
Common	DRD2		19
Unique	DRD2 v1		4
Common	DRD3		3
NoSplice	DRD4		6
NoSplice	DRD5		3
NoSplice	DUSP1		4
Common	DUSP10		3
Unique	DUSP10 v1		13
NoSplice	DUSP11		2
NoSplice	DUSP12		11
NoSplice	DUSP13		8
NoSplice	DUSP14		12
Common	DUSP15		16
NoSplice	DUSP18		6
NoSplice	DUSP19		6
NoSplice	DUSP22		4
NoSplice	DUSP3		23
Common	DUSP4		1
Junction	DUSP4v1		30
NoSplice	DUSP5		5
NoSplice	DUSP7	•	29
NoSplice	DUSP8		13
NoSplice	E2IG5		2
NoSplice	EAF1		13
NoSplice	EAT2		3
NoSplice	EBAG9		3
NoSplice	EBI2		5
NoSplice	ED1		12
NoSplice	EDN2		5
Mochine	1 4 C	5.6	ŭ

Housekeeping	EEF1G		27
NoSplice	EFNA1		55
NoSplice	EFNA2		3
-	EFNA3		34
NoSplice			16
NoSplice	EFNA5		4
NoSplice	EFNB1		
NoSplice	EFNB2		8
NoSplice	EFNB3		17
NoSplice	EGF		7
NoSplice	EGFR		5
NoSplice	EGR1		13
NoSplice	El24		12
NoSplice	ELK1		4
NoSplice	EMR1		3
NoSplice	EN1		3
NoSplice	EN2		12
NoSplice	ENO1		39
NoSplice	ENSA		5
-	EPHA1		14
NoSplice	EPHA2		5
NoSplice			3
NoSplice	EPHA3		5
NoSplice	EPHA4		
NoSplice	EPHA5		10
NoSplice	EPHA7		13
NoSplice	EPHA8		35
NoSplice	EPHB1		6
Common	EPHB2		7
NoSplice	EPHB3		10
NoSplice	EPHB4		56
NoSplice	EPHX2		3
NoSplice	EPS15		6
NoSplice	EPS15R		8
NoSplice	ERBB2		4
NoSplice	ERBB3		11
-	ESR1		19
NoSplice	ESR2		20
NoSplice			14
NoSplice	ESRRA		3
NoSplice	ESRRB		5
NoSplice	ETS1		3
NoSplice	FADD		
NoSplice	FADS1		5
Common	FAF1		3
Unique	FAF1 v1		3
NoSplice	FCGBP		15
NoSplice	FCGR1A		6
NoSplice	FCGRT		4
Common	FGF1		4
Unique	FGF1 v1		10
NoSplice	FGF2		21
NoSplice	FGF3		4
NoSplice	FIGF		9
Moshince	1 101		_

NoSplice	FKBP1A	1
Common	FKBP1B	10
Unique	FKBP1B v1	5
Junction	FKBP1B v2	2
NoSplice	FKBP2	15
NoSplice	FKBP3	5
NoSplice	FKBP4	30
NoSplice	FKBP5	5
NoSplice	FKBP6	5
NoSplice	FKBP8	13
NoSplice	FLJ12541	21
NoSplice	FLT3	10
NoSplice	FLT3LG	5
NoSplice	FOS	18
NoSplice	FOXA1	27
NoSplice	FOXA2	1
NoSplice	FOXA3	7
NoSplice	FOXP3	8
NoSplice	FSHB	12
NoSplice	FSHR	4
Housekeeping-mismatch	FTL	44
Housekeeping	FTL	11
· =	FURIN	6
NoSplice	FUS	45
NoSplice	FYB	11
NoSplice	GAB1	8
NoSplice		13
Common	GAB2	4
Unique	GAB2 v1	17
NoSplice	GABARAP	18
Common	GABBR1	3
NoSplice	GABRA1	11
NoSplice	GABRA2	7
NoSplice	GABRA3	8
NoSplice	GABRA4	
NoSplice	GABRA5	20
NoSplice	GABRA6	16
NoSplice	GABRB1	29
NoSplice	GABRD	14
NoSplice	GABRG2	10
NoSplice	GABRG3	7
NoSplice	GABRP	15
NoSplice	GABRQ	6
NoSplice	GABRR1	9
NoSplice	GABRR2	 6
Common	GAD1	3
NoSplice	GAD2	9
NoSplice	GADD45A	11
NoSplice	GADD45G	12
NoSplice	GALR1	34
NoSplice	GALR2	38
NoSplice	GALR3	13

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Housekeeping	GAPD	13
NoSplice	GATA3	15
NoSplice	GBP1	14
NoSplice	GBP2	7
NoSplice	GBP4	18
NoSplice	GBP5	2
NoSplice	GCG	3
Common	GCK	4
NoSplice	GCKR	15
NoSplice	GDF10	4
NoSplice	GDNF	9
NoSplice .	GFAP	20
·	GFRA1	13
Common	GFRA2	4
NoSplice	GFRA3	5
NoSplice		6
NoSplice	GGTLA1	13
NoSplice	GHITM	15
NoSplice	GHRHR	5
NoSplice	GHSR	7
NoSplice	GIOT-3	
NoSplice	GLRA1	5
Common	GMEB1	5
Junction	GMEB1v1	2 2
Junction	GMEB1v2	
NoSplice	GMEB2	7
NoSplice	GMFB	18
NoSplice	GMFG	5
NoSplice	GNAS	3
NoSplice	GNRH1	10
NoSplice	GNRHR	4
NoSplice	GPB5	2
NoSplice	GPHA2	5
NoSplice	GPHN	15
NoSplice	GPR10	17
NoSplice	GPR14	3
NoSplice	GPR17	8
NoSplice	GPR2	1
NoSplice	GPR24	6
NoSplice	GPR30	35
NoSplice	GPR39	9
NoSplice	GPR48	8
NoSplice	GPR49	7
NoSplice	GPR50	7
NoSplice	GPR51	11
NoSplice	GPR57	7
NoSplice	GPR58	4
NoSplice	GPR66	3
NoSplice	GPR81	5
NoSplice	GPX1	6
NoSplice	GRAP2	3
NoSplice NoSplice	GRB7	21
Moohing	50	

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Common	GREB1		3
Unique	GREB1 va		15
NoSplice	GRIA1		7
NoSplice	GRIA2		10
NoSplice	GRIA4		8
NoSplice	GRID2		12
NoSplice	GRIN2D		3
NoSplice	GRM1		5
NoSplice	GRM2		18
NoSplice	GRM3		3
NoSplice	GRM5		7
NoSplice	GRM6		7
NoSplice	GRM7		7
NoSplice	GRM8		5
NoSplice	GRPR		30
NoSplice	GRTP1		17
NoSplice	GSR		14
NoSplice	GSTA3		3
NoSplice	GSTM3		3
NoSplice	GZMM	· ·	3
NoSplice	HAL		23
NoSplice	HARC		3
NoSplice	HCRT		4
NoSplice	HCRTR1		6
NoSplice	HCRTR2		12
NoSplice	HDAC3		13
NoSplice	HDC		11
NoSplice	HGF		11
NoSplice	HGFAC		3
NoSplice	HGS		6
NoSplice	HIP1		17
NoSplice	HK2		4
NoSplice	HLA-A		1
NoSplice	HLA-B		1
NoSplice	HLA-DNA		3
Housekeeping	HLA-DOA		3
NoSplice	HLA-DQA1		10
NoSplice	HLA-DRB1		3
NoSplice	HLALS		3
NoSplice	HM74		6
NoSplice	HMOX1		2
NoSplice	HMOX2		3
NoSplice	HOXA1		6
NoSplice	HOXB1		5
NoSplice	HRH1		9
NoSplice	HRH2		15
NoSplice	HRH3		52
NoSplice	HSD11B1		9
NoSplice	HSD11B2		3
NoSplice	HSD17B3		3
NoSplice	HSD17B8		8
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NoSplice	HSF1	3
NoSplice	HSOBRGRP	3
NoSplice	HSP105B	13
NoSplice	HSPA1A	3
NoSplice	HSPA1L	8
NoSplice	HSPA2	3
NoSplice	HSPA4	5
NoSplice	HSPA5	3
NoSplice	HSPA6	19
Common	HSPA8	7
NoSplice	HSPA9B	40
NoSplice	HSPB1	3
NoSplice	HSPB2	6
NoSplice	HSPB3	3
NoSplice	HSPB7	4
NoSplice	HSPC228	3
NoSplice	HSPCA	3
NoSplice	HSPCB	4
NoSplice	HSPD1	7
NoSplice	HTR1A	24
NoSplice	HTR1B	14
NoSplice	HTR1D	11
NoSplice	HTR1F	8
NoSplice	HTR2A	18
NoSplice	HTR2B	7
NoSplice	HTR2C	27
NoSplice	HTR3A	9
NoSplice	HTR4	4
NoSplice	HTR6	4
Common	HTR7	3
NoSplice	IAN4L1	3
NoSplice	ICAM5	11
NoSplice	ICSBP1	15
NoSplice	IDE	18
NoSplice	IFI35	8
NoSplice	1F144	3
NoSplice	IFIT1	1
NoSplice	IFIT2	12
NoSplice	IFRD1	6
NoSplice	IFRD2	3
NoSplice	IGF1	6
NoSplice	IGF1R	7
NoSplice	IGF2	8
NoSplice	IGFBP2	5
NoSplice	IGFBP3	9
NoSplice	IGFBP4	41
NoSplice	IGFBP5	3
NoSplice	IKBKAP	13
NoSplice	IKBKB	6
NoSplice	IKBKE	39
NoSplice	IKBKG	6
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NoSplice	IL-17RC	4
Common	IL-17RE	8
NoSplice	IL-23R	3
NoSplice	IL10RB	5
Common	IL11RA	15
NoSplice	IL12B	11
NoSplice	IL12RB2	1
NoSplice	IL13RA1 ,	3
NoSplice	IL13RA2	1
NoSplice	IL15	7
NoSplice	IL16	3
NoSplice	IL17	2
NoSplice	IL17B	8
NoSplice	IL17BR	6
NoSplice	IL17E	3
NoSplice	IL17R	7
NoSplice	IL18BP	5
NoSplice	IL18RAP	7
NoSplice	IL19	1
NoSplice	IL1B	7
NoSplice	IL1R1	9
NoSplice	IL1RAPL1	8
NoSplice	IL1RAPL2	16
NoSplice	IL20RA	8
NoSplice	IL21R	6
NoSplice	IL22	7
NoSplice	IL22R	6
NoSplice	IL24	1
NoSplice	IL28RA	2
NoSplice	IL2RA	ა 9
NoSplice	IL2RB	4
NoSplice	IL2RG	3
NoSplice	IL6ST	14
NoSplice	IL8RB	10
NoSplice	ILF1	3
NoSplice	ILF2	11
Common	ILF3	16
NoSplice	INHA	9
NoSplice	INHBA	4
NoSplice	INHBC INS	16
NoSplice	INSIG1	13
NoSplice	INSIG2	3
NoSplice	INSM1	32
NoSplice NoSplice	INSR	12
NoSplice	IPF1	8
NoSplice	IRAK1	3
NoSplice	IRAK2	7
NoSplice	IRAK3	8
NoSplice	IRF1	16
NoSplice	IRF2	13
Hoopiloo	· · · · =	

NoSplice	IRF4		23
MultiVar	IRF5		18
NoSplice	. IRF6		12
MultiVar	IRF7		4
NoSplice	IRS1		6
NoSplice	IRS2		3
NoSplice	IRS4		10
NoSplice	ISGF3G		8
NoSplice	ITGA1		13
NoSplice	ITGA2		4
NoSplice	ITGA3		3
NoSplice	ITGA4		8
NoSplice	ITGA5		44
NoSplice	ITGA6		6
NoSplice	ITGAL		13
NoSplice	ITGAM		5
NoSplice	ITGAX		9
NoSplice	ITK		57
NoSplice	ITM2B		16
NoSplice	JAK1		9
NoSplice	JAK2		7
NoSplice	JAK3		6
NoSplice	JAM2		11
NoSplice	JUN		27
NoSplice	JUNB		4
NoSplice	KIT	•	6
NoSplice	KLF16		4
NoSplice	KLK2		1
NoSplice	KPNB2		7
NoSplice	LAT		2
NoSplice	LCK		16
NoSplice	LCN7		3
NoSplice	LCP1		4
NoSplice	LCP2		25
NoSplice	LEC2		29
NoSplice	LEP		18
NoSplice	LEPR		4
NoSplice	LGALS3BP		7
NoSplice	LHCGR		17
NoSplice	LHX3		2
NoSplice .	LIF		3
NoSplice	LIFR		10
NoSplice	LIPE		16
NoSplice	LNPEP		3
NoSplice	LOC134728		19
NoSplice	LOC152503		6
NoSplice	LOC55971		11
NoSplice	LOC56920		3
NoSplice	LRBA		17
MultiVar	LRDD		3
NoSplice	LTA		12
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NoSplice	LTA4H	11
MultiVar	LTB	8
NoSplice	LTB4R	5
NoSplice	LTB4R2	18
NoSplice	LTBR	1
Arabidopsis-biotinylated	LTP4	16
Arabidopsis	LTP6	18
MultiVar	MADD	30
NoSplice	MAFF	2
NoSplice	MAGED1	6
NoSplice	MAOA	6
NoSplice	MAOB	21
NoSplice	MAP2K1	34
MultiVar	MAP2K3	13
NoSplice	MAP2K4	4
MultiVar	MAP2K6	34
MultiVar	MAP2K7	13
NoSplice	MAP3K10	9
NoSplice	MAP3K11	3
NoSplice	MAP3K12	3
NoSplice	MAP3K13	4
NoSplice	MAP3K2	8
NoSplice	MAP3K3	11
MultiVar	MAP3K4	12
MultiVar	MAP3K7	29
NoSplice	MAP3K8	17
NoSplice	MAP4K1	8
NoSplice	MAP4K3	5
MultiVar	MAPK1	1
MultiVar	MAPK10	16
NoSplice	MAPK13	3
MultiVar	MAPK14	17
MultiVar	MAPK8	18
NoSplice	MAPK8IP1	3
MultiVar	MAPK8IP2	3
MultiVar	MAPK9	32
MultiVar	MAPKAPK2	6
MultiVar	MASP1	4
MultiVar	MASP2	32
MultiVar	MATK	29
NoSplice	MAZ	9
•	MBP	17
NoSplice	MC1R	6
NoSplice	MC2R	3
NoSplice	MC3R	24
NoSplice		8
NoSplice	MC4R	1
NoSplice	MDK	7
NoSplice	MEF2C	, 18
NoSplice	MEIS2	14
NoSplice	MET	6
NoSplice	MHC2TA	O

NoSplice	MIF	5
NoSplice	MIG-6	11
NoSplice	MIZIP	12
NoSplice	MKNK2	71
NoSplice	MME	11
NoSplice	MMP2	8
NoSplice	MMP3	8
NoSplice	MMP8	39
NoSplice	MMP9	11
NoSplice	MPL	10
NoSplice	MS4A3	2
NoSplice	MST1	4
NoSplice	MST1R	6
NoSplice	MT2A	1
NoSplice	MT3	13
NoSplice	MTNR1B	7
NoSplice	MX2	8
NoSplice	MYC	14
NoSplice	MYD88	3
NoSplice	N-PAC	12
NoSplice	NAALAD2	1
Arabidopsis	NAC1	14
NoSplice	NCAM1	4
MultiVar	NCOA1	52
NoSplice	NCOA2	11
NoSplice	NCOA3	6
NoSplice	NCOA4	14
NoSplice	NCOA5	7
NoSplice	NCOA6	32
NoSplice	NCOA6IP	5
NoSplice	NCSTN	10
NoSplice	NELL2	17
NoSplice	NFATC1	2
NoSplice	NFATC3	15
NoSplice	NFIL3	1
NoSplice	NFKB1	15
NoSplice NoSplice	NFKB2	5
NoSplice	NFKBIA	42
NoSplice	NFKBIE	3
NoSplice	NFKBIL1	7
NoSplice	NFRKB	5
MultiVar	NFX1	16
NoSplice	NGFB	29
NoSplice	NGFR	6
NoSplice	NGFRAP1	2
NoSplice	NMB	4
NoSplice	NMBR	6
NoSplice	NOS1	7
MultiVar	NOS2A	12
NoSplice	NOS3	7
NoSplice	NOSIP	12
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NoSplice	NOSTRIN	10
NoSplice	NPFF	10
NoSplice	NPPC	2
MultiVar	NPR2	68
NoSplice	NPR3	20
NoSplice	NPY1R	2
NoSplice	NPY2R	11
NoSplice	NPY5R	7
NoSplice	NR0B1	10
NoSplice	NR1	4
NoSplice	NR1D1	5
NoSplice	NR1D2	4
NoSplice	NR1H2	3
NoSplice	NR1H3	3
NoSplice	NR1H4	2
MultiVar	NR1I2	13
NoSplice	NR2C1	13
NoSplice	NR2C2	5
NoSplice	NR2E1	14
NoSplice	NR2F1	3
NoSplice	NR2F2	4
NoSplice	NR2F6	3
NoSplice	NR3C1	20
NoSplice	NR3C2	. 9
NoSplice	NR4A1	5
NoSplice	NR4A2	16
NoSplice	NR4A3	6
NoSplice	NR5A1	4
NoSplice	NR5A2	8
NoSplice	NR6A1	10
NoSplice	NRBF-2	6
NoSplice	NRF	7
MultiVar	NRG1	11
MultiVar	NRG2	26
NoSplice	NRGN	11
NoSplice	NRIP1	10
NoSplice	NRP2	10
NoSplice	NRTN	5
NoSplice	NS	3
NoSplice	NSEP1	3
NoSplice	NTF3	3
NoSplice	NTF5	10
NoSplice	NTRK1	22
NoSplice	NTRK2	3
NoSplice	NTRK3	10
NoSplice	NTS	21
NoSplice	NTSR2	7
NoSplice	NTT5	4
NoSplice	NTT73	9
NoSplice	NXPH1	5
NoSplice	NYREN18	, 8
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NoSplice NoSplice NoSplice NoSplice NoSplice NoSplice NoSplice NoSplice	OAT ODC1 OPRK1 OT7T022 OXT OXTR P38IP		12 5 3 8 5 23 4
NoSplice NoSplice NoSplice	PACE4 PADI5 PAK1		4 4 5 4
NoSplice NoSplice	PAPPA PC		8
NoSplice	PCSK1		11
NoSplice	PCSK1N		18
NoSplice	PCSK2		12
MultiVar	PDCD4		16
MultiVar	PDGFA		4
NoSplice	PDGFB		3 5
NoSplice	PDGFC		5 8
NoSplice	PDGFRA PDGFRB		9
NoSplice	PDGFRL		1
NoSplice NoSplice	PECAM1		4
NoSplice	PER1		7
MultiVar	PER2		12
NoSplice	PER3		8
NoSplice	PERC		7
NoSplice	PGDS		4
NoSplice	PGR		4
NoSplice	PGRMC1		6
NoSplice	PGRMC2		8
NoSplice	PI4K2B		28
NoSplice	PIAS1		12
NoSplice	PIGR		7
NoSplice	PIK3CG		10 10
NoSplice	PLA2G4A		10
NoSplice	PLA2G6 PLA2R1		9
NoSplice MultiVar	PLAC3		54
NoSplice	PLG		3
NoSplice	PLTP		3
NoSplice	PLXNB1		5
NoSplice	PLXNC1		30
NoSplice	PMCH		10
NoSplice	PMCHL1		14
NoSplice	PMX2B		10
NoSplice	PNMT		4
NoSplice	PNOC		4
NoSplice	PNR		3
NoSplice	POLE4		7
NoSplice	POMC	65	3

NoSplice POR 20 NoSplice PPARD 12 NoSplice PPARD 5 NoSplice PPARGC1 13 MultiVar PPM1D 20 NoSplice PPM1D 20 NoSplice PPPHR1B 14 NoSplice PPPR1 11 NoSplice PREB 32 NoSplice PREB 32 NoSplice PREB 32 NoSplice PRKCA 5 NoSplice PRKCB1 16 NoSplice PRKCB1 16 NoSplice PRKCB 7 NoSplice PRKCB 7 NoSplice PRKRIR 5 Arabidopsis PRKAS 5 NoSplice PRS11 25 NoSplice PRS11 25 NoSplice PRS4 4 MultiVar PSCD2 49 NoSplice PSEM1 5 NoS	NoSplico	POR		20
NoSplice PPARD 5 NoSplice PPARGC1 13 MultiVar PPM1A 31 NoSplice PPM1D 20 NoSplice PPPHR1B 14 NoSplice PPPHR1B 14 NoSplice PPPR1B 11 NoSplice PRED 32 NoSplice PREB 32 NoSplice PREB 32 NoSplice PRKCA 5 NoSplice PRKCB1 16 NoSplice PRKCD 11 NoSplice PRKCD 11 NoSplice PRKCE 7 NoSplice PRKRIR 5 Arabidopsis PRKase 18 NoSplice PRKR 2 NoSplice PRKA 5 NoSplice PRX 5 NoSplice PSEM1 5 MultiVar PSSMB9 4 NoSplice PTCH2 3 No	-			
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NoSplice PTPN4 13	MultiVar	PTPN22		
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MultiVar PTPN6 27	NoSplice	PTPN4		
	MultiVar	PTPN6		27

MultiVar	PTPN7			19
NoSplice	PTPN9			7
NoSplice	PTPNS1			7
MultiVar	PTPRC			14
NoSplice	PTPRK			7
NoSplice	PTPRN			43
NoSplice	PTX3			13
NoSplice	RAF1			13
NoSplice	RAG1			10
NoSplice	RAG2			9
NoSplice	RAI			7
•	RAMP2			1
NoSplice	RAMP3			6
NoSplice	RARA			36
NoSplice				7
MultiVar	RARB			5
NoSplice	RARRES3			4
NoSplice	RASD1			3
NoSplice	RBP2			15
Arabidopsis	RCA			
Arabidopsis	RCP1			15
NoSplice	RDC1			5
NoSplice	REA			10
NoSplice	RELB			12
NoSplice	RFC1			12
NoSplice	RFRP			5
MultiVar	RFX2			3
NoSplice	RFXAP			10
NoSplice	RGC32			19
NoSplice	RGN			6
NoSplice	RGS19IP1			23
NoSplice	RGS9			19
NoSplice	RNPEPL1			5
NoSplice	RODH			9
NoSplice	RORA			12
NoSplice	RORB			6
NoSplice	RORC			30
Housekeeping	RPL10A			24
Housekeeping	RPL37A			22
NoSplice	RPS10			3
Housekeeping	RPS21			12
NoSplice	RPS5			14
NoSplice	RTN1			18
NoSplice	RTN2			11
NoSplice	RTN3			3
NoSplice	RTN4			5
NoSplice	RXRA			54
NoSplice	RXRB			26
NoSplice	RelA			13
NoSplice	SAMHD1			3
NoSplice	SCAMP2			16
NoSplice	SCAP1			2
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NoSplice	SCAP2		10
NoSplice	SCG2		28
NoSplice	SCGN		8
NoSplice	SCN1A		8
NoSplice	SCN1B		16
NoSplice	SCN2A2		3
NoSplice	SCN2B		20
NoSplice	SCN3A		3
NoSplice	SCN4A		39
NoSplice	SCN5A		8
NoSplice	SCN7A		15
NoSplice	SCN9A		6
NoSplice	SCP2		3
NoSplice	SCT		4
NoSplice	SCYE1		13
NoSplice	SELE		6
NoSplice	SELPLG .		6
NoSplice	SEMA3A		20
NoSplice	SEMA3B		3
NoSplice	SEMA3C		3
NoSplice	SEMA3D	ı	13
NoSplice	SEMA3E		15
NoSplice	SEMA3F		9
NoSplice	SEMA4C		3
NoSplice	SEMA4D		6
NoSplice	SEMA4F		8
NoSplice	SEMA4G		8
NoSplice	SEMA5A		9
NoSplice	SEMA5B		4
NoSplice	SEMA6A		9
MultiVar	SEMA6B		9
MultiVar	SEMA6D		17
NoSplice	SEMA7A		9
NoSplice	SERPINA6		2
NoSplice	SERPINE1		14
NoSplice	SFRS5		3
MultiVar	SGKL		5
NoSplice	SGNE1		3
NoSplice	SHARP		6
NoSplice	SHBG		7
NoSplice	SHC1		36
NoSplice	SHC3		17
NoSplice	SIGLEC5		1
NoSplice	SITPEC		9
NoSplice	SLC11A1		6
NoSplice	SLC11A2		14
NoSplice	SLC15A2		8
NoSplice	SLC18A1		6
NoSplice	SLC18A2		7
NoSplice	SLC18A3		3
NoSplice	SLC1A1		16
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NoSplice	SLC1A2		18
NoSplice	SLC1A3		24
NoSplice	SLC21A2		6
NoSplice	SLC22A3		12
NoSplice	SLC22A5		3
NoSplice	SLC25A20		25
MultiVar	SLC25A3		3
NoSplice	SLC25A4		7
NoSplice	SLC25A5		12
NoSplice	SLC29A1		4
NoSplice	SLC2A4		3
NoSplice	SLC6A1		61
NoSplice	SLC6A11		32
NoSplice	SLC6A12		31
NoSplice	SLC6A13		5
NoSplice	SLC6A14		24
NoSplice	SLC6A2		17
NoSplice	SLC6A3		6
NoSplice	SLC6A4		4
NoSplice	SLC6A5		8
NoSplice	SLC6A6		4
NoSplice	SLC6A7		28
NoSplice	SLC6A8		23
NoSplice	SLC6A9		4
MultiVar	SMARCA2		39
NoSplice	SMARCA4		26
MultiVar	SMARCF1		86
MultiVar	SNAP23		12
NoSplice	SNAP29		2
NoSplice	SNT-1		17
NoSplice	SNT-2		10
NoSplice .	SNW1		8
MultiVar	SNX15		2
NoSplice	SNX4		21
MultiVar	SNX6		2
NoSplice	SOCS1		13
NoSplice	SOCS2		38
NoSplice	SOCS3		6
NoSplice	SOD2		16
NoSplice	SPC		2
MultiVar	SPINT1		2
NoSplice	SPINT2		6
NoSplice	SPN		2
NoSplice	SPP1		6
MultiVar	SR-BP1		1
NoSplice	SRC		28
NoSplice	SRY		1
NoSplice	SSBP1		4
NoSplice	SST		7
MultiVar	STAT1		23
NoSplice	STAT2		4
		51	

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MultiVar	STAT3	25
NoSplice	STAT4	10
NoSplice	STAT5A	23
MultiVar	SYN1	41
MultiVar	SYN2	37
MultiVar	SYN3	6
MultiVar	TAC1	6
MultiVar	TACR1	13
MultiVar	TAF9	11
MultiVar	TBXAS1	17
MultiVar	TCIRG1	28
NoSplice	TFE3	31
NoSplice	TFRC	5
NoSplice	TGFA	8
NoSplice	TGFB1	3
NoSplice	TGFB2	10
NoSplice	TGFB3	5
NoSplice	THPO	13
NoSplice	THRA	12
NoSplice	THRB	3
NoSplice	THRSP	14
NoSplice	TIAF1	7
Arabidopsis	TIM	10
NoSplice	TIMELESS	8
NoSplice	TIMM23	7
NoSplice	TIMP2	7
NoSplice	TIMP3	17
NoSplice	TIMP4	5
MultiVar	TIRAP	3
NoSplice	TLOC1	5
NoSplice	TLR1	3
NoSplice	TLR2	13
NoSplice	TLR3	13
NoSplice	TLR5	3
NoSplice	TLR6	15
NoSplice	TLR7	17
MultiVar	TLR8	15
NoSplice	TMSB4X	17
NoSplice	TNFRSF11A	7
NoSplice	TNFRSF11B	7
MultiVar	TNFRSF19	9
NoSplice	TNFRSF19L	5
NoSplice	TNFRSF1A	4
NoSplice	TNFRSF1B	12
NoSplice	TNFRSF21	4
NoSplice	TNFRSF4	3
MultiVar	TNFRSF6B	3
MultiVar	TNFSF12	6
NoSplice	TNFSF13	2
NoSplice	TNFSF13B	13
NoSplice	TNFSF15	2
Noophoo	77.1.0.10	

NoSplice	TNFSF5	•	1
NoSplice	TNFSF6		3
NoSplice	TNFSF8		3
NoSplice	TOMM70A		8
NoSplice	TP53		7
NoSplice	TPH		7
NoSplice	TPT1		18
MultiVar	TRADD		1
NoSplice	TRAF1		11
MultiVar	TRAF2		2
MultiVar	TRAF3		31
NoSplice	TRAF6		7
NoSplice	TRAP100		8
NoSplice	TRAP150		3
NoSplice	TRAP240		16
NoSplice	TRHDE		11
NoSplice	TRHR		13
NoSplice	TRIAD3		13
NoSplice	TRIM		2
NoSplice	TRIP		10
NoSplice	TRIP10		3
NoSplice	TRIP11		6
NoSplice	TRIP12		12
NoSplice	TRIP13		3
NoSplice	TRIP15		7
NoSplice	TRIP3		5
NoSplice	TRIP4		9
MultiVar	TRO		25
NoSplice	TRP		38
NoSplice	TRPM2		6
NoSplice	TSHB		10
NoSplice	TSHR		8
NoSplice	TXNIP		6
NoSplice	TYK2		5
NoSplice	UBC		2
NoSplice	UBP1	•	16
NoSplice	UCHL1		11
NoSplice	UCN		2
NoSplice	UGTREL1		21
NoSplice	VAMP2		35
NoSplice	VDAC1		3
NoSplice	VDAC2		3
NoSplice	VDAC3		30
NoSplice	VDR		7
NoSplice	VIAAT		7
NoSplice	VIPR1		13
NoSplice	VIPR2		3
NoSplice	VSNL1	•	11
NoSplice	WAS		8
NoSplice	WASF1		20
MultiVar	WISP1	70	∠ U

NoSplice	WISP2		8
NoSplice	WNT1		3
NoSplice	WNT10B		12
NoSplice	WNT2		4
MultiVar	WSB1		18
Arabidopsis	XCP2		13
NoSplice	XCR1		6
NoSplice	YARS	No.	13
NoSplice	YWHAB		4
NoSplice	ZAP-70		17
NoSplice	ZFP36		7
NoSplice	ZFP36L1		6
NoSplice	ZIC2		4
NoSplice	ZNF147		5
NoSplice	ZNF161		7
NoSplice	ZNF259		6
NoSplice	ZNF398		3
NoSplice	pknbeta		17
Arabidopsis	rbcL		13
NoSplice	sod1		11

5. Example 5

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Dysregulation of the concerted action of nervous, endocrine and immune 175. systems has been observed in several medically explained diseases, and implicated in 5 several illnesses which are still unexplained. These medically unexplained illnesses are typically multifactorial in nature, defined only by symptoms, and have anatomic lesions which are inaccessible or have not been found (Wessely S 1999). One particularly inaccessible region is the brain, which plays a central role in the pyschoneuroendocrine-immune (PNI) processes. Many human studies have by necessity used 10 postmortem tissue or brain-derived cell lines, which are limited either in terms of sample availability and quality, or relevance to in vivo function. Animal models validating the molecular cross-talk between the mind and the body are more advanced than human studies, in part because brain, endocrine and immune samples can be obtained more readily, but questions remain as to their representation of human 15 pathophyisiology. New methods for monitoring PNI communication, and the capacity of an individual to maintain healthy PNI homeostasis, would therefore be of great interest to the medical and scientific communities.

176. Peripheral blood is potentially an ideal sample for profiling PNI gene expression due to its circulation throughout the body, including leukocyte trafficking across the blood brain barrier. Even though low levels of peripheral blood

mononuclear cell (PBMC) gene expression variability have been detected, most of the variability can be attributed to individual contributions of age and sex (Campbell C 2002; Whitney AR 2003). The remarkable lack of variability in peripheral blood gene expression within healthy age and sex-matched populations provides an important gauge of health, and serves as a baseline for measuring peripheral blood gene expression associated with illness. There are several examples where the peripheral blood has been used to detect differential gene expression when there is no known or accessible lesion including inflammatory diseases (Heller RA 1997), neurological injury (Tang Y 2003), and chronic fatigue syndrome (Vernon 2002).

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177. Herein, PNI peripheral blood gene expression was assessed by first building an annotated database of 1,622 genes known to be involved in neuroendocrine and immune pathways, then querying peripheral blood-specific databases generated from expressed sequence tag (EST) data and microarray experiments. Expression of 1,058 of the 1,622 PNI genes (65% coverage) was identified in the peripheral blood and a noteworthy number of neural and endocrine genes whose expression was unanticipated.

a) Methods & Materials

(1) PNI database:

A customized Microsoft Access database of genes encoding proteins 178. that participate in biosynthetic, biochemical, and regulatory pathways of the nervous, endocrine and immune systems was generated and annotated to include gene name and Refseq abbreviation, Genbank Accession number, UniGene identification, functional information, alternate gene names, and both protein and nucleic acid sequences. The genes included in this database were selected by soliciting suggestions from molecular biologists, immunologists, endocrinologists, neurologists and psychiatrists. Published reviews covering such subjects as hypothalamic-pituitary-adrenal (HPA) axis functioning, cytokine signaling, and the complement pathways were surveyed for additional relevant genes. Both Biocarta (http://www.biocarta.com/) and Kegg (http://www.genome.ad.jp/kegg/kegg4.html) pathway databases were utilized. Redundancies were eliminated and the list extended by keyword searches of the Refseq database using words such as "immune", "hormone", "neuroendocrine", "glucocorticoid", "neurotransmitter", "T-cell", among others. Gene abbreviations were standardized to the National Center for Biotechnology Information (NCBI) RefSeq

nomenclature. Although inclusion in the list was necessarily subjective, every attempt was made to be systematic. For example, if a gene was included in the list due to known protein function, related genes (paralogs) that are less well understood were also included. Similarly, genes were included if they were shown to regulate, or be regulated by, important molecular signals. The Refseq abbreviation, UniGene number, System and Category for the complete list of genes in the PNI database, along with whether its expression was detected in the EST database, the peripheral blood microarray database or both is provided as a Table 8.

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(2) Peripheral blood EST database:

A search for libraries that had been prepared from normal (non-neoplastic) human blood samples in NCBI's GenBank EST database (dbEST)

(http://www.ncbi.nlm.nih.gov/dbEST/) produced nine EST libraries (see Table 6).

Table 6: The cDNA libraries used to construct the peripheral blood EST database.

Library name (UniGene Library ID)	Source	ESTs in library	Classified in UniGene	UniGene clusters represented
RA-MO-I (498)	Monocytes	6	2	2
Soares_NPBMC (6295)	Lymphocyte	2113	1951	1597
NIH_MGC_106 (6351)	Natural killer cells, cell line	6407	5928	2261
Proliferating Erythroid Cells (824)	Primary culture- Erythroid Cells	721	639	430
Homo Sapiens cDNA Library from Peripheral White Blood Cell (5009)	Peripheral White Blood Cells	3	0	Ó
Proliferating Human Erythroid Cells (6899)	Primary culture- Erythroid Cells	5182	4153	1624
Human Platelet (143)	Platelet	9	8	8
NIH MGC 118 (6925)	White blood cells	10533	9397	4464
Human White blood cells (129)	White blood cells	934	905	677
RA-MO-III (238)	Monocytes	5	2	2
Human peripheral blood (242)	Whole peripheral blood	8	8	4
Red blood cell (483)	Red blood cell	65	63	4

GenBank®'s annotated EST sequences were downloaded and reformatted into an MS Access database. The entries contained 25,986 sequences, of which 23,056 could be

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classified as belonging to one of 7,655 UniGene clusters. Analysis of PNI expression in this database was performed using MS Access to match UniGene ID numbers.

(3) Peripheral blood microarray database:

Gene expression in the peripheral blood mononuclear cells (PBMCs) of 179. twelve individuals (six male, six female) was examined using the Human 10K A, B and C microarrays (MWG Biotech, Inc., High Point, North Carolina). These volunteers were participating in a clinical study into the causes of chronic fatigue syndrome (CFS), and eight were CFS patients while four were normal controls. Extraction of total RNA, synthesis of the biotinylated cDNA probe, hybridization to these microarrays, and detection using resonance light scattering has been described (Ojaniemi H 2003)(Ojaniemi et al, 2003). The scanned TIFF images were processed using ArrayVisionTM (Imaging Research Inc., Ontario, Canada) to measure signal intensity and background for each feature. This data was extracted into an MS Access database. Datapoints which were uninformative due to technical issues were flagged and removed from subsequent analysis. A partial list of UniGene cluster IDs corresponding to specific oligos was supplied by MWG Biotech, along with Gene Ontology (GO) categories for each oligo. Of 13,074 non-redundant UniGene cluster IDs unambiguously corresponding to specific oligos, 1,281 matched to genes in PNI database. Analysis of PNI expression in PMBCs was limited to these 1,281 PNI genes in the microarray database and positive gene expression was defined as a signal-tonoise ratio greater than 2.5 in at least 75% (9 of 12) of the samples.

(4) Gene categorization:

180. Each gene in the PNI database was categorized according to its system and subcategorized by known or suspected protein function using information summarized by Genbank or Online Mendelian Inheritance in Man (OMIM, http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM) where possible where possible, or from the primary literature.

b) Results

181. A total of 1,622 non-redundant genes representing nervous (16%; 263/1622), endocrine (20%; 323/1622), and immune (38%; 618/1622) systems were identified for inclusion in the PNI database (Table 7). Genes in the "other" category (26%; 418/1622) had well characterized roles in multiple systems, or were important because of their regulatory characteristics. The 1,622 PNI genes included

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neurotransmitters, hormones, and cytokines, which are principal signaling molecules of these systems. Multiple transcriptional products representing functional regulation at the RNA level were encoded by one hundred and eighty-seven of these, distributed proportionately (±8%) to the overall distribution.

182. To determine the extent of peripheral blood PNI gene expression, both the EST and microarray databases were queried. There were 566 genes from the EST database that matched to one of the 1,622 genes in the PNI database (Table 7). Half of these genes (51%; 289/566) had immune function while smaller fractions represented neural (6%; 34/566) and endocrine functions (13%; 72/566). Of the 30,000 genes represented by oligonucleotides on the microarrays, 1,281 could be matched to genes in the annotated PNI database. There was positive hybridization to 764 of the 1,281 (60%) PNI genes (Table 7). It was confirmed that at least two out of the four samples derived from normal control volunteers showed positive hybridization for every gene reported as expressed. The proportions of genes in the neural (18%; 135/764), endocrine (19%; 145/764), immune (36%; 278/764), and "other" (27%; 206/764) categories whose peripheral blood expression was detected on microarrays was similar to these categories in PNI database.

Table 7: The categories and distribution of PNI genes in the three databases.

***************************************			icroarray I	
System	Category	Database Da	atabase I	<u>Database</u>
Endocrine	Hormone Metabolism	81	33	17
	Hormone Receptor	94	43	12
	Hormones	45	22	1
	Regulated by Hormones	29	15	11
	Regulates Hormone Activity	55	20	25
	Regulates Hormone Expression	19	12	6
Immune	Apoptosis	44	17	30
•	Complement Component	30	18	8
	Cytokine/Chemokine Receptors	90	44	38
	Cytokines/Chemokines	108	57	31
	Immune: MHC/HLA	22	4	20
	Other Immune Function	287	123	147
	Regulated by Cytokines	9	5	4
	Regulates Cytokine Activity	22	10	8
	T-cell Activation	6	0	3
Nervous	Amyloid processing	18	12	7
	Neurotransmitter	19	12	0
	Neurotransmitter Metabolism	33	16	10
	Neurotransmitter Receptor	101	44	3
	Other Neural Function	37	19	3

***************************************	Regulated by Neurotransmitters	2	1	1
	Regulates Neurotransmitter Activity	51	29	10
	Regulates Neurotransmitter			
	Expression	2	2	0
Other	Circadian	7	4	4
	Growth Factor	27	13	5
	Growth Factor Receptor	13	5	2
	Heat shock	20	8	11
	Homeostasis & Small Molecule			
	transport	37	18	6
	Other	18	10	10
	Other Neuroendocrine Function	34	20	12
	Protease Inhibitor	9	3	4
	Regulation of Cell Growth	63	28	18
	Signal Transduction	76	40	41
	Stress Response	10	4	9
	Transcription Factor	100	50	46
	Unknown Function	4	3	3
	Total	1622	764	566

183. Peripheral blood expression of several noteworthy neural and endocrine genes was detected. Sequences representing both the γ-aminobutyric acid type B (GABA_(B)) neurotransmitter receptor and γ-aminobutyric acid type A receptor-associated protein (GABARAP) were identified in the peripheral blood EST database. Microarrays detected peripheral blood expression of six GABAergic genes. Three of these belong to the GO functional grouping "GABA-A receptor activity", one in the GO group "GABA-B receptor activity" and two in the GO group "GABA\:sodium symporter activity".

184. Peripheral blood expression of many hormone receptors was detected solely in the PBMC microarray database, including progesterone receptor membrane component 2 (PGRMC2), oxytocin receptor (OXTR), prolactin receptor (PRLR), and thirty-nine other genes which are categorized in the PNI annotation as having known or probable hormone receptor activity. Thirty three genes belonging to the GO functional group "hormone activity" were found to be expressed in PBMCs including oxytocin, leptin, and proopiomelanocortin(POMC). Expression of progesterone receptor membrane component 1 (PGRMC1) was detected both in the EST database and the PBMC microarray database. Genes that modulate hormonal response, such as zinc finger protein 147 (ZNF147, also known as Efp or estrogen-responsive finger protein)

were also detected. The complete list of neural and endocrine gene expression in the peripheral blood can be found in Table 8.

c) Discussion

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- 185. If changes in the PNI response detectable in peripheral blood can be correlated to specific physiologic states, insights could be gained about many complex diseases with suspected PNI dysregulation simply be analyzing gene expression profiles in blood. Accordingly, the possibility of peripheral blood gene expression of a comprehensive set of PNI genes was investigated.
- 186. Evidence for peripheral blood neurotransmitter activity was seen in both the EST and microarray databases. Microarray expression of dopaminergic receptors D1, D3, and D5 (DRD1, DRD3, DRD5) and the dopamine transporter (solute carrier family 6, member 3, abbreviated SLC6A3) was observed, in agreement with earlier findings of dopamine receptors present on lymphocytes (Amenta F 1999) and of direct activity of dopamine on T-cells (Levite M 2001). Peripheral blood expression of the beta-2- adrenergic receptor (ADRB2), a norepinephine receptor that has a well-documented role in regulating immunity (Sanders 2002), and nicotinic cholinergic receptor beta polypeptide 1 (CHRNB1), an acetylcholine receptor which was previously identified as expressed on T and B cells (Hiemke 1996; Toyabe 1997) was also confirmed.
- 187. The finding of GABA receptors and transporters in peripheral blood suggests the existence of a previously unstudied systemic GABAergic response. Participation of the (GABA)ergic system in immunomodulation has long been recognized (Devoino 1992), and the role of GABA_(A) receptors in stimulating release of hypothalamic and pituitary hormones in response to cytokine activity has been well described (McCann 2000). A more direct role was suggested by the discovery of a functional GABA_(A) receptor on the surface of T cells (Tian 1999). However, details about the role of GABAergic proteins in peripheral blood remain to be determined.
- 188. Of the hormone receptors found in peripheral blood, the presence of membrane-associated progesterone receptor PGRMC1 is particularly interesting. The rat homolog has been shown by differential display PCR to be expressed in the hypothalamus and to regulate female reproductive behavior (Krebs 2000). Other genes were of interest due to their potential to be induced by hormonal activity in certain tissues. One of these was ZNF147, which is up-regulated by estrogen and down-

regulated by transforming growth factor- [Inoue 1993; Inoue 1999]. ZNF147 acts by targeting the 14-3-3sigma protein for proteolysis (Urano 2002). Since 14-3-3sigma sequesters BCL2-associated X protein (Bax) (Samuel 2001), which plays an essential role in T-cell development (Bouillet 2002), the expression of this gene in peripheral blood can represent a direct mechanism for endocrine influence on immune function. While expression of this gene was observed in fewer than 75% of the samples by microarray, and thus defined as "unexpressed", it appears to be differentially expressed depending on gender (data not shown).

189. Many of the genes in the PNI database have well-understood roles in the immune, nervous, or endocrine systems, and were categorized accordingly. Since the immunological function of PBMCs is well established, the predominance of immune system genes in the both databases was understood. However, microarray analysis of PBMCs revealed more neural and endocrine gene expression then anticipated with similar distribution of genes in each category of the PNI database as a whole. The criteria for positive hybridization on microarrays is stringent making it unlikely that expression of the genes in the neural and endocrine categories is due to noise. Importantly, many of the neuroendocrine gene expression levels were high reflecting a much larger role of the peripheral blood in PNI signaling than previously recognized and support PNI profiling of the peripheral blood to provide clues to the communication between the brain and the body.

Table 8: PNI genes and their peripheral blood expression

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RefSeq	UniGene		E. data a second
Abbreviation	Cluster ID System	Category	Evidence
AANAT	Hs.152972 Endocrine	Hormone Metabolism	
ACE	Hs.298469 Endocrine	Hormone Metabolism	Microarray
AKR1C3	Hs.78183 Endocrine	Hormone Metabolism	EST
ALDH1A1	Hs.76392 Endocrine	e Hormone Metabolism	
ALDH1A2	Hs.95197 Endocrine	e Hormone Metabolism	
ALDH1A3	Hs.75746 Endocrine	e Hormone Metabolism	
ALDH1B1	Hs.169517 Endocrine	e Hormone Metabolism	Both Databases
ALDḤ2	Hs.195432 Endocrine	e Hormone Metabolism	Both Databases
ALDH3A2	Hs.159608 Endocrine	e Hormone Metabolism	Both Databases
ALDH3B1	Hs.83155 Endocrine	e Hormone Metabolism	EST
ALDH3B2	Hs.87539 Endocrine	e Hormone Metabolism	
ALDH4A1	Hs.77448 Endocrine	e Hormone Metabolism	EST
ALDH6A1	Hs.293970 Endocrine	e Hormone Metabolism	
ALDH7A1	Hs.74294 Endocrine	e Hormone Metabolism	Both Databases
ALDH8A1	Hs.18443 Endocrine	e Hormone Metabolism	Microarray
ALDH9A1	Hs.2533 Endocrine	e Hormone Metabolism	Both Databases
BZRP	Hs.202 Endocrine	e Hormone Metabolism	Both Databases

CETP	Hs.89538 Endocrine		Microarray
CYP11A	Hs.76205 Endocrine		Microarray
CYP11B1	Hs.377912 Endocrine		•
CYP11B2	Hs.184927 Endocrine		
CYP17A1		Hormone Metabolism	Microarray
CYP19		Hormone Metabolism	Microarray
CYP1A1	Hs.72912 Endocrine	Hormone Metabolism	Both Databases
CYP1A2		Hormone Metabolism	
CYP1B1		Hormone Metabolism	
CYP21A2	Hs.278430 Endocrine	Hormone Metabolism	
CYP24	Hs.89663 Endocrine	Hormone Metabolism	Microarray
CYP26A1	Hs.150595 Endocrine	Hormone Metabolism	
CYP27A1	Hs.82568 Endocrine	Hormone Metabolism	Both Databases
CYP27B1	Hs.199270 Endocrine	Hormone Metabolism	Both Databases
CYP2A13	Hs.181973 Endocrine	Hormone Metabolism	
CYP2A6	Hs.334345 Endocrine	Hormone Metabolism	
CYP2A7	Hs.250615 Endocrine	Hormone Metabolism	
CYP2B6	Hs.1360 Endocrine	Hormone Metabolism	Microarray
CYP2C18	Hs.702 Endocrine	Hormone Metabolism	
CYP2C19	Hs.198501 Endocrine	Hormone Metabolism	
CYP2C8	Hs.174220 Endocrine	Hormone Metabolism	
CYP2C9	Hs.167529 Endocrine	Horrnone Metabolism	
CYP2D6	Hs.333497 Endocrine	Hormone Metabolism	Microarray
CYP2E1	Hs.75183 Endocrine	Hormone Metabolism	Microarray
CYP2F1	Hs.72913 Endocrine	Hormone Metabolism	
CYP2J2	Hs.152096 Endocrine	Hormone Metabolism	Microarray
CYP2S1	Hs.98370 Endocrine	Hormone Metabolism	EST
CYP39A1	Hs.20766 Endocrine	Hormone Metabolism	
CYP3A4	Hs.178738 Endocrine	Hormone Metabolism	
CYP3A43	Hs.306220 Endocrine	Hormone Metabolism	
CYP3A5	Hs.104117 Endocrine	Hormone Metabolism	
CYP3A7	Hs.172323 Endocrine	Hormone Metabolism	
CYP46	Hs.25121 Endocrine	Hormone Metabolism	Microarray
CYP4A11	Hs.1645 Endocrine	Hormone Metabolism	
CYP4B1	Hs.687 Endocrine	Hormone Metabolism	Microarray
CYP4F11	Hs.187393 Endocrine	Hormone Metabolism	
CYP4F12	Hs.180570 Endocrine	Hormone Metabolism	
CYP4F2	Hs.101 Endocrine	Hormone Metabolism	
CYP4F3	Hs.106242 Endocrine	Hormone Metabolism	Microarray
CYP4F8	Hs.268554 Endocrine	Hormone Metabolism	Microarray
CYP51	Hs.226213 Endocrine	Hormone Metabolism	•
CYP7A1	Hs.1644 Endocrine	Hormone Metabolism	
CYP7B1	Hs.144877 Endocrine	Hormone Metabolism	
CYP8B1		Hormone Metabolism	•
DIO1		Hormone Metabolism	Microarray
DIO2		Hormone Metabolism	Microarray
DIO3		Hormone Metabolism	Microarray
EDN2		Hormone Metabolism	Microarray
GSTA3		Hormone Metabolism	-
HSD11B1		Hormone Metabolism	
AND THE PERSON NAMED OF THE PERSON	Maria de la composição de	~~~~\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	我在我的现在分词的"这个中心的我们"的说,我们的时候就会对了他们的人,但一个人的人的人的人,我们就是一个人的对方的人,他们是一个人的人的人,他们也是一个人的人 "

HSD11B2		Hormone Metabolism	
HSD17B1		Hormone Metabolism	Misus suppl
HSD17B3		Hormone Metabolism	Microarray
HSD17B8		Hormone Metabolism	EST ·
HSD3B1		Hormone Metabolism	3 4
LIPE		Hormone Metabolism	Microarray
POR		Hormone Metabolism	EST
PTGIS		Hormone Metabolism	
RODH		Hormone Metabolism	Microarray
STS		Hormone Metabolism	
SULT1A3		Hormone Metabolism	EST
SULT2A1		Hormone Metabolism	
TBXAS1		Hormone Metabolism	Both Databases
TPO	Hs.2041 Endocrine	Hormone Metabolism	Microarray
ADCYAP1R1	Hs.377783 Endocrine	Hormone Receptor	
AGTRL2	Hs.433156 Endocrine	Hormone Receptor	
AMHR2	Hs.123014 Endocrine	Hormone Receptor	Microarray
AR	Hs.99915 Endocrine	Hormone Receptor	
AVPR1A	Hs.2131 Endocrine	Hormone Receptor	
AVPR1B		Hormone Receptor	
AVPR2		Hormone Receptor	Microarray
CCKAR		Hormone Receptor	Microarray
CNTFR	Hs.194774 Endocrine		
CRHR1	Hs.79117 Endocrine		
CRHR2	Hs.66578 Endocrine		Microarray
EMR1		Hormone Receptor	
EMR2	Hs.137354 Endocrine		Microarray
EMR3	Hs.326777 Endocrine		
ESR1		Hormone Receptor	Microarray
ESR2	Hs.103504 Endocrine		Microarray
ESRRA	Hs.110849 Endocrine		EST
ESRRB	Hs.337489 Endocrine		
FSHR		Hormone Receptor	
GHRHR		Hormone Receptor	Microarray
GHSR	Hs.248115 Endocrine		Microarray
GNRHR	Hs.73064 Endocrine		Microarray
GNRHR2	Hs.356873 Endocrine		
GPR14	Hs.192720 Endocrine		Microarray
GPR24	Hs.248122 Endocrine		Microarray
	Hs.248124 Endocrine		•
GPR31	Hs.248126 Endocrine		Microarray
GPR38	Hs.377914 Endocrine		
GPR39		Hormone Receptor	
GPR48		e Hormone Receptor	
GPR49		Hormone Receptor	
GPR50		Hormone Receptor	Microarray
GPR51		Hormone Receptor	
GPR57		Hormone Receptor	
GPR58		Hormone Receptor	Microarray
GPR66			
GPR81	⊓S.3207 12 Endocrine	e Hormone Receptor	

***************************************			Micrograv
GRIN2D	Hs.113286 Endocrine		Microarray
HSOBRGRP	Hs.23581 Endocrine		
INSR	Hs.89695 Endocrine		
LEC2	Hs.107054 Endocrine		
LEPR	Hs.226627 Endocrine		
LHCGR		Hormone Receptor	
LOC152503	Hs.24715 Endocrine		
MC1R	Hs.380388 Endocrine	-	
MC2R	Hs.248144 Endocrine		• ••
MC3R	Hs.248018 Endocrine		Microarray
MC4R	Hs.247980 Endocrine	•	Microarray
MC5R	Hs.248145 Endocrine	Hormone Receptor	Microarray
MTNR1A	Hs.248147 Endocrine		
MTNR1B	Hs.158328 Endocrine		
NR0B1	Hs.268490 Endocrine	Hormone Receptor	Microarray
NR0B2	Hs.427055 Endocrine	Hormone Receptor	
NR1D2	Hs.37288 Endocrine	Hormone Receptor	
NR1H2	Hs.100221 Endocrine	Hormone Receptor	Both Databases
NR1H3	Hs.347353 Endocrine	Hormone Receptor	Microarray
NR1H4	Hs.171683 Endocrine	Hormone Receptor	Microarray
NR2C1	Hs.108301 Endocrine		
NR2C2	Hs.378877 Endocrine	Hormone Receptor	
NR2E1	Hs.22591 Endocrine	Hormone Receptor	
NR2E3	Hs.187354 Endocrine		
NR2F1	Hs.421993 Endocrine		
NR2F2	Hs.347991 Endocrine	Hormone Receptor	. "
NR2F6	Hs.239752 Endocrine		Microarray
NR3C1	Hs.75772 Endocrine		Both Databases
NR3C2		Hormone Receptor	
NR4A1		Hormone Receptor	Both Databases
NR4A2	Hs.82120 Endocrine		Both Databases
NR4A3	Hs.80561 Endocrine		Both Databases
NR5A1	Hs.157037 Endocrine		Microarray
NR5A2	Hs.183123 Endocrine		
NR6A1	Hs.278599 Endocrine		Microarray
OXTR		Hormone Receptor	Microarray
PGR		Hormone Receptor	•
PGRMC1		Hormone Receptor	Both Databases
PGRMC2		Hormone Receptor	Both Databases
PHIP		Hormone Receptor	
PRLR		Hormone Receptor	Microarray
PTHR1		Hormone Receptor	;
PTHR2		Hormone Receptor	Microarray
RARA		Hormone Receptor	EST
RARB		Hormone Receptor	Microarray
			Ť
			Microarray
			Microarray
			Both Databases
RDC1 RORA RORB RORC RXRA	Hs.23016 Endocrine Hs.2156 Endocrine Hs.198481 Endocrine Hs.133314 Endocrine	Hormone Receptor Hormone Receptor Hormone Receptor Hormone Receptor Hormone Receptor Hormone Receptor	Microarray Microarray

RXRB	Hs.79372 Endocrine		Both Databases
SLT	Hs.333173 Endocrine	Hormone Receptor	
TACR1	Hs.1080 Endocrine	Hormone Receptor	
THRA	Hs.724 Endocrine	Hormone Receptor	Microarray
THRB	Hs.121503 Endocrine	Hormone Receptor	
TRHR	Hs.3022 Endocrine	Hormone Receptor	Microarray
TSHR	Hs.123078 Endocrine	Hormone Receptor	Microarray
VIPR1	Hs.348500 Endocrine		EST
ADM		Hormones	EST
AMH	Hs.112432 Endocrine	Hormones	Microarray
AVP	Hs.89648 Endocrine	Hormones	Microarray
CCKBR	Hs.203 Endocrine	Hormones	Microarray
CGA	Hs.119689 Endocrine		Microarray
CHGA	Hs.172216 Endocrine		Microarray
CHGB		Hormones	Microarray
CNTF	Hs.348372 Endocrine		·
CRH	Hs.75294 Endocrine		Microarray
EPO		Hormones	Microarray
FSHB	Hs.36975 Endocrine		•
GCG	Hs.399996 Endocrine		
	Hs.115352 Endocrine		
GH1	Hs.378728 Endocrine		
GH2	Hs.37023 Endocrine		Microarray
GHRH			Mioroarray
GNRH1	Hs.82963 Endocrine Hs.129715 Endocrine		Microarray
GNRH2			Mioroarray
GPHA2	Hs.127223 Endocrine		Microarray
HCRT	Hs.158348 Endocrine		Microarray
INHA		Hormones	
INHBA		Hormones	
INHBC	Hs.374664 Endocrine		
INS	Hs.89832 Endocrine		Missassus
INSL3	Hs.37062 Endocrine		Microarray
INSL5	Hs.251380 Endocrine		Microarray
INSL6	Hs.147467 Endocrine		B 41
LEP	Hs.194236 Endocrine		Microarray
LHB	Hs.154704 Endocrine		h a*
OXT	Hs.113216 Endocrine		Microarray
PMCH	• • • • • • • • • • • • • • • • • • • •	Hormones	
PMCHL1	Hs.247975 Endocrine		
PMCHL2	Hs.381277 Endocrine	Hormones	
POMC	Hs.1897 Endocrine	Hormones	Microarray
PRL	• • • • • • •	Hormones	Microarray
PTH	Hs.37045 Endocrine		Microarray
PTHLH	Hs.89626 Endocrine	Hormones	Microarray
RETN	Hs.283091 Endocrine		
RLN1	Hs.105314 Endocrine	Hormones	Microarray
RLN2	Hs.127032 Endocrine	Hormones	
RLN3	Hs.352155 Endocrine	Hormones	
SCT	Hs.302005 Endocrine	Hormones	
SPC	Hs.343668 Endocrine	Hormones	Microarray

	100004 5 15 25	11	Microarray
TRH	Hs.182231 Endocrine		Microarray
TSHB	Hs.406687 Endocrine		
UCN	Hs.134932 Endocrine		
AIG-1		Regulated by Hormones	EST
CDK4		Regulated by Hormones	
CDKN1C		Regulated by Hormones	Microarray
E2IG2		Regulated by Hormones	Microarray
E2IG4		Regulated by Hormones	Microarray
E2IG5		Regulated by Hormones	EST
EBAG9		Regulated by Hormones	Microarray
FLJ12541		Regulated by Hormones	Microarray
FSHPRH1		Regulated by Hormones	Microarray
GHITM		Regulated by Hormones	EST
GREB1		Regulated by Hormones	Microarray
GRTP1		Regulated by Hormones	
HK2		Regulated by Hormones	Microarray
HSPB1		Regulated by Hormones	Both Databases
INSIG1		Regulated by Hormones	EST
INSIG2		Regulated by Hormones	
LCN7	Hs.173508 Endocrine	Regulated by Hormones	
NRGN	Hs.26944 Endocrine	Regulated by Hormones	
NS	Hs.279923 Endocrine	Regulated by Hormones	EST
PIP	Hs.99949 Endocrine	Regulated by Hormones	Microarray
PSCD2	Hs.303091 Endocrine	Regulated by Hormones	EST
RARRES1		Regulated by Hormones	Microarray
RARRES2		Regulated by Hormones	Microarray
RARRES3		Regulated by Hormones	EST
RASD1		Regulated by Hormones	Both Databases
SFRS5	Hs.166975 Endocrine	Regulated by Hormones	EST
SRY	Hs.1992 Endocrine	Regulated by Hormones	Microarray
THRSP		Regulated by Hormones	
TOMM70A		Regulated by Hormones	Both Databases
ABCB1	Hs.21330 Endocrine	Regulates Hormone Activity	
ADRB1	Hs.99913 Endocrine	Regulates Hormone Activity	
AGRP		Regulates Hormone Activity	
ALB		Regulates Hormone Activity	
ASIP		Regulates Hormone Activity	
CALR		Regulates Hormone Activity	EST
COASTER		Regulates Hormone Activity	EST
CREBBP		Regulates Hormone Activity	
CRHBP		Regulates Hormone Activity	Microarray
FKBP4		Regulates Hormone Activity	Both Databases
GMEB1		Regulates Hormone Activity	
GNAS		Regulates Hormone Activity	EST
GPB5		Regulates Hormone Activity	
IDE		Regulates Hormone Activity	EST
IRS1		Regulates Hormone Activity	Microarray
IRS2		Regulates Hormone Activity	
IRS2 IRS4		Regulates Hormone Activity	
MKNK2		Regulates Hormone Activity	Both Databases
MININI	135.20 TOZO E, NOOTHIC	/ Regulated Hermital / Restrict	

MME	Hs.1298 Endocrine	Regulates Hormone Activity	
NCOA2		Regulates Hormone Activity	
NCOA3	Hs.225977 Endocrine	Regulates Hormone Activity	EST
NCOA4	Hs.99908 Endocrine	Regulates Hormone Activity	EST
NCOA5	Hs.288140 Endocrine	Regulates Hormone Activity	
NCOA6	Hs.159613 Endocrine	Regulates Hormone Activity	
NCOA6IP	Hs.179909 Endocrine	Regulates Hormone Activity	EST
NRBF-2	Hs.27181 Endocrine	Regulates Hormone Activity	EST
PCSK1N	Hs.429437 Endocrine	Regulates Hormone Activity	
PERC	Hs.248652 Endocrine	Regulates Hormone Activity	
PI4K2B	Hs.23920 Endocrine	Regulates Hormone Activity	Microarray
PLAC3	Hs.293896 Endocrine	Regulates Hormone Activity	Microarray
PRDM2		Regulates Hormone Activity	EST
PTPN1		Regulates Hormone Activity	Both Databases
RBP2		Regulates Hormone Activity	
REA		Regulates Hormone Activity	Both Databases
RGS19IP1		Regulates Hormone Activity	Microarray
SHARP		Regulates Hormone Activity	Both Databases
SHBG		Regulates Hormone Activity	Microarray
SIGLEC6		Regulates Hormone Activity	Microarray
SNX15		Regulates Hormone Activity	Both Databases
SNX4		-	EST
		Regulates Hormone Activity	EST
SNX6		Regulates Hormone Activity	
SP110		Regulates Hormone Activity	Both Databases
ST13		Regulates Hormone Activity	EST
TRAP100		Regulates Hormone Activity	Both Databases
TRAP150		Regulates Hormone Activity	EST
TRAP240		Regulates Hormone Activity	N.41
TRHDE		Regulates Hormone Activity	Microarray
TRIP10		Regulates Hormone Activity	Microarray
TRIP11		Regulates Hormone Activity	Both Databases
TRIP12		Regulates Hormone Activity	EST
TRIP13		Regulates Hormone Activity	Microarray
TRIP15		Regulates Hormone Activity	EST
TRIP3		Regulates Hormone Activity	
TRIP4		Regulates Hormone Activity	Both Databases
UGT2B7	Hs.10319 Endocrine	Regulates Hormone Activity	
ENSA	Hs.111680 Endocrine	Regulates Hormone Expression	Both Databases
GALR2	Hs.158351 Endocrine	Regulates Hormone Expression	Microarray
GALR3	Hs.158353 Endocrine	Regulates Hormone Expression	
HDAC3	Hs.446552 Endocrine	Regulates Hormone Expression	
INHBB	Hs.1735 Endocrine	Regulates Hormone Expression	
IPF1	Hs.32938 Endocrine	Regulates Hormone Expression	Microarray
KLK1		Regulates Hormone Expression	Microarray
KLK2		Regulates Hormone Expression	Microarray
LHX3		Regulates Hormone Expression	Microarray
NCOA1		Regulates Hormone Expression	Both Databases
NRIP1		Regulates Hormone Expression	EST
PC		Regulates Hormone Expression	Microarray
PCSK1		Regulates Hormone Expression	······································
1 OOK	113.10011		

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PCSK2		Regulates Hormone Expression	Deth Detahases
PREB	Hs.279784 Endocrine	Regulates Hormone Expression	Both Databases
PRH		Regulates Hormone Expression	Microarray
SMARCA4		Regulates Hormone Expression	Both Databases
SNW1		Regulates Hormone Expression	EST
SST	Hs.12409 Endocrine	Regulates Hormone Expression	Microarray
AKT1	Hs.71816 Immune	Apoptosis	Both Databases
APAF1	Hs.373575 Immune	Apoptosis	
APCS	Hs.1957 Immune	Apoptosis	Microarray
ASC	Hs.71869 Immune	Apoptosis	EST
BAK1	Hs.93213 Immune	Apoptosis	Both Databases
BAX	Hs.159428 Immune	Apoptosis	EST
BCL2	Hs.79241 Immune	Apoptosis	Both Databases
BCL2A1	Hs.227817 Immune	Apoptosis	EST
BCL2L1	Hs.305890 Immune	Apoptosis	EST
BCL2L2	Hs.75244 Immune	Apoptosis	Both Databases
BID	Hs.172894 Immune	Apoptosis	Both Databases
BTN3A1	Hs.284283 Immune	Apoptosis	EST
CARD10	Hs.57973 Immune	Apoptosis	Microarray
CASP1	Hs.2490 Immune	Apoptosis	
CASP10	Hs.5353 Immune	Apoptosis	
CASP2	Hs.108131 Immune	Apoptosis	
CASP3	Hs.74552 Immune	Apoptosis	Both Databases
CASP4	Hs.74122 Immune	Apoptosis	Both Databases
CASP5	Hs.3257 Immune	Apoptosis	Microarray
CASP6	Hs.3280 Immune	Apoptosis	•
CASP7	Hs.9216 Immune	Apoptosis	
CASP8	Hs.381231 Immune	Apoptosis	EST
CASP9	Hs.100641 Immune	Apoptosis	EST
CFLAR	Hs.195175 Immune	Apoptosis	EST
DAP	Hs.75189 Immune	Apoptosis	EST
DAPK1	Hs.153924 Immune	Apoptosis	EST
El24	Hs.343911 Immune	Apoptosis	EST
	Hs.86131 Immune	Apoptosis	EST
FADD	Hs.25821 Immune	Apoptosis	EST
FAF1	Hs.239706 Immune	Apoptosis	
GAB1		Apoptosis	
ICEBERG	Hs.56279 Immune	Apoptosis	
LRDD	Hs.123136 Immune	• •	Both Databases
MADD	Hs.82548 Immune	Apoptosis	EST
MAGED1	Hs.177556 Immune	Apoptosis	Both Databases
MYD88	Hs.82116 Immune	Apoptosis	Both Databases
TANK	Hs.146847 Immune	Apoptosis	EST
TIAF1	Hs.75822 Immune	Apoptosis	Both Databases
TNFSF6	Hs.2007 Immune	Apoptosis	EST
TP53	Hs.1846 Immune	Apoptosis	Microarray
TRADD	Hs.89862 Immune	Apoptosis	Both Databases
TRAF1	Hs.2134 Immune	Apoptosis	EST
TRAF2	Hs.373508 Immune	Apoptosis	EST
VDAC1	Hs.149155 Immune	Apoptosis	Microarray
WISP1	Hs.194680 Immune	Apoptosis	wiici carray

BF	Hs.69771 Immune	Complement Component	
C1QA	Hs.9641 Immune	Complement Component	
C1QB	Hs.8986 Immune	Complement Component	Microarray
C1QBP	Hs.78614 Immune	Complement Component	Both Databases
C1QR1	Hs.97199 Immune	Complement Component	Both Databases
C1R	Hs.1279 Immune	Complement Component	
C1S	Hs.169756 Immune	Complement Component	
C2	Hs.2253 Immune	Complement Component	Both Databases
C3	Hs.284394 Immune	Complement Component	Microarray
C4A	Hs.170250 Immune	Complement Component	Microarray
C4B	Hs.433721 Immune	Complement Component	
C4BPA	Hs.1012 Immune	Complement Component	Microarray
C4BPB	Hs.99886 Immune	Complement Component	Microarray
C5	Hs.1281 Immune	Complement Component	Microarray
C5R1	Hs.2161 Immune	Complement Component	Microarray
C6	Hs.1282 Immune	Complement Component	
C7	Hs.78065 Immune	Complement Component	Microarray
C8A	Hs.93210 Immune	Complement Component	Microarray
C8B	Hs.38069 Immune	Complement Component	
C8G	Hs.1285 Immune	Complement Component	
C9	Hs.1290 Immune	Complement Component	Microarray
CLU	Hs.75106 Immune	Complement Component	EST
CR1	Hs.193716 Immune	Complement Component	Microarray
CR2	Hs.73792 Immune	Complement Component	Both Databases
DF	Hs.155597 Immune	Complement Component	Both Databases
ITGAM	Hs.172631 Immune	Complement Component	EST
MASP1	Hs.356082 Immune	Complement Component	
MASP2	Hs.119983 Immune	Complement Component	Microarray
MBL2	Hs.2314 Immune	Complement Component	Microarray
RGC32	Hs.76640 Immune	Complement Component	EST
BLR1	Hs.113916 Immune	Cytokine/Chemokine Receptors	Both Databases
	Hs.117572 Immune	Cytokine/Chemokine Receptors	Microarray
CCBP2		Cytokine/Chemokine Receptors	Both Databases
CCR1	Hs.301921 Immune	•	Microarray
CCR2	Hs.395 Immune	Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors	Both Databases
CCR3	Hs.158324 Immune	·	DOIN Databases
CCR4	Hs.184926 Immune	Cytokine/Chemokine Receptors	
CCR5	Hs.54443 Immune	Cytokine/Chemokine Receptors	
CCR6	Hs.46468 Immune	Cytokine/Chemokine Receptors	Both Databases
CCR7	Hs.1652 Immune	Cytokine/Chemokine Receptors	DOIN Dalabases
CCR8	Hs.113222 Immune	Cytokine/Chemokine Receptors	Missosus
CCR9	Hs.225946 Immune	Cytokine/Chemokine Receptors	Microarray
CCRL1	Hs.310512 Immune	Cytokine/Chemokine Receptors	h 4:
CCRL2	Hs.302043 Immune	Cytokine/Chemokine Receptors	Microarray
CMKLR1	Hs.159553 Immune	Cytokine/Chemokine Receptors	Microarray
CRL3	Hs.351813 Immune	Cytokine/Chemokine Receptors	D-0- D (-1
CSF1R	Hs.174142 Immune	Cytokine/Chemokine Receptors	Both Databases
CSF2RA	Hs.182378 Immune	Cytokine/Chemokine Receptors	
CSF2RB	Hs.285401 Immune	Cytokine/Chemokine Receptors	
CSF3R	Hs.2175 Immune	Cytokine/Chemokine Receptors	Both Databases
CX3CR1	Hs.78913 Immune	Cytokine/Chemokine Receptors	Both Databases

CXCR3 Hs.198252 Immune CXCR6 Hs.384526 Immune FY Hs.183 Immune GPR17 Hs.48453 Immune GPR2 Hs.278446 Immune GPR30 Hs.113207 Immune It.10RA Hs.1375555 Immune It.17RR Hs.29539 Immune It.17RR Hs.21544 Immune It.17RC Hs.29539 Immune It.17RC Hs.29530 Immune It.17RC Hs.29530 Immune It.17RC Hs.29530 Immune It.17RC Hs.29530 Immune It.1812 Hs.25333 Immune It.1812 Hs.25331 Immune It.1814 Hs.266 Immune It.22RA Hs.25454 Immune It.22RA Hs.25545 Immune It.22RA Hs.25545 Immune It.22RA Hs.25545 Immune It.22RA Hs.25546 Immune It.22RA Hs.375184 Immune It.22RA Hs.375184 Immune It.22RA Hs.375184 Immune It.28RA Hs.375331 Immune It.28RA Hs.375476 Immune It.28RA Hs.375476 Immune It.28RA Hs.375476 Immune It.28RA Hs.375476 Immune It.28RA Hs.376347 Immune It.28RA Hs.375476 Immune It.28RA Hs.375476 Immune It.28RA Hs.376347 Immune				**************************************
CXCR8 Hs.34526 Immune FY Hs.183 Immune GPR37 Hs.46453 Immune GPR2 Hs.278446 Immune GPR30 Hs.113207 Immune IL10RA Hs.327 Immune IL10RB Hs.173936 Immune IL10RB Hs.173936 Immune IL11RA Hs.64310 Immune IL12RB1 Hs.121544 Immune IL13RA1 Hs.285115 Immune IL13RA2 Hs.25954 Immune IL13RA1 Hs.25954 Immune IL17RR Hs.12751 Immune IL17RR Hs.12751 Immune IL17RR Hs.129751 Immune IL17RR Hs.3277 Immune IL17RR Hs.129751 Immune IL17R Hs.31524 Immune IL17RB1 Hs.129751 Immune IL17RB2 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB3 Hs.25333 Immune IL17RB2 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB1 Hs.129751 Immune IL17RB2 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB4 Hs.129751 Immune IL17RB5 Hs.31524 Immune IL17RB2 Hs.31524 Immune IL17RB4 Hs.31524 Immune IL17RB5 Hs.31524 Immune IL17RB4 Hs.32751 Immune IL17RB5 Hs.31524 Immune IL17RB4 Hs.31524 Immune IL17RB5 Hs.31524 Immune IL17RB4 Hs.31524 Immune IL17RB5 Hs.31524 Immune IL17RB4 Hs.31524 Immune IL17RB5 Hs.31524 Immune IL17RB5 Hs.3109415 Immune IL17RB5 Hs.31524 Immune IL17RB5 Hs.31634 Immune IL2RB4 Hs.31634 Immune IL2RBA Hs.363334 Immune IL2RBA Hs.363334 Immune IL2RBA Hs.368376 Immune IL2RB Hs.1702 Immune IL3RBA Hs.1702 Immune IL5RBA	CXCR3	Hs.198252 Immune		Both Databases
FY	CXCR4	Hs.89414 Immune	Cytokine/Chemokine Receptors	
GPR17 Hs.46453 Immune GPR2 Hs.278446 Immune GPR30 Hs.113207 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Both Databases Both Databases Cytokine/Chemokine Receptors Cytoki	CXCR6	Hs.34526 Immune	Cytokine/Chemokine Receptors	Microarray
GPR2 Hs.278446 Immune GPR30 Hs.13207 Immune GPR30 Hs.13207 Immune IL10RA Hs.137655 Immune IL10RA Hs.327 Immune IL10RB Hs.173936 Immune IL11RA Hs.64310 Immune IL12RB1 Hs.125954 Immune IL17RC Hs.129591 Immune IL17RC Hs.129540 Immune IL17RL Hs.25833 Immune IL17RL Hs.25331 Immune IL1RL1 Hs.21654 Immune IL1RL2 Hs.25844 Immune IL1RL2 Hs.25854 Immune IL1RL3 Hs.25854 Immune IL1RR Hs.158301 Immune IL1RR Hs.158301 Immune IL1RR Hs.158301 Immune IL1RR Hs.158301 Immune IL1RR Hs.21054 Immune IL1RR Hs.2668 Immune IL1RR Hs.2668 Immune IL2RR Hs.12868 Immune IL2RR Hs.1686 Immune IL2RR Hs.1762 Immune IL2RR Hs.1686 Immune IL2RR Hs.17689 Immune IL2RR Hs.17689 Immune IL2RR Hs.1866 Immune IL2RR Hs.1867 Immune IL2RR Hs.193400 Immune IL4RR Hs.1940 Immune IL5RR Hs.1702 Immune IL5RR Hs.1710 Imm	FY	Hs.183 Immune	Cytokine/Chemokine Receptors	
GPR30 Hs.113207 Immune HM74 Hs.137555 Immune L10RA Hs.3275 Immune L110RB Hs.173936 Immune L111RA Hs.64310 Immune L111RA Hs.64310 Immune L112RB1 Hs.121644 Immune L113RA1 Hs.285115 Immune L113RA1 Hs.285115 Immune L113RA2 Hs.28514 Immune L117RB Hs.5470 Immune L117RC Hs.12959 Immune L117RC Hs.12959 Immune L117RC Hs.12959 Immune L117RC Hs.29595 Immune L11R1 Hs.66 Immune L11RL1 Hs.66 Immune L11RL2 Hs.2533 Immune L11RL2 Hs.2633 Immune L11RL2 Hs.2634 Immune L11RL3RA1 Hs.2533 Immune L11RL Hs.86 Immune L12RA Hs.1680 Immune L12RA Hs.12864 Immune L12RA Hs.12868 Immune L12RA Hs.375184 Immune L12RA Hs.375184 Immune L12RA Hs.4728 Immune L12RA Hs.7545 Immune L12RA Hs.75545 Immune L12RA Hs.75546 Immune L12RA Hs.75546 Immune L12RA Hs.75545 Immune L12RA Hs.75546 Immune L12RA Hs.75545 Immune L12RA Hs.75545 Immune L12RA Hs.75546 Immune L12RA Hs.75546 Immune L12RA Hs.75545 Immune L12RA Hs.75546 Immune L12RA Hs.75547 Immune L12RA Hs.75546 Immune L12RA Hs.75547 Immune L12RA Hs.86876 Immune L12RA Hs.	GPR17	Hs.46453 Immune		
HM74 Hs.137555 Immune IL10RA Hs.327 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Both Databases Both Databases Soth Databases Soth Databases Soth Databases Soth Databases Both Databases Soth Databases Hs.17861 Immune Ls.285115 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Rece	GPR2	Hs.278446 Immune	Cytokine/Chemokine Receptors	Microarray
L10RA	GPR30	Hs.113207 Immune		
Li10RA	HM74	Hs.137555 Immune	Cytokine/Chemokine Receptors	
IL11RA	IL10RA	Hs.327 Immune	Cytokine/Chemokine Receptors	
Li-12RB-1	IL10RB	Hs.173936 Immune	Cytokine/Chemokine Receptors	
L12RB2	IL11RA	Hs.64310 Immune	Cytokine/Chemokine Receptors	•
IL13RA1 Hs.285115 Immune IL13RA2 Hs.25954 Immune IL15RA Hs.12503 Immune IL15RA Hs.12503 Immune IL17RR Hs.12575 Immune IL17RR Hs.129751 Immune IL17RC Hs.129959 Immune IL-17RE Hs.31524 Immune IL-17RE Hs.31524 Immune IL18R1 Hs.359301 Immune IL1R1 Hs.82112 Immune IL1R2 Hs.25333 Immune IL1R2 Hs.25333 Immune IL1RL1 Hs.66 Immune IL1RL2 Hs.102865 Immune IL2RA Hs.210546 Immune IL2RA Hs.126891 Immune IL2RA Hs.375184 Immune IL2RA Hs.3753184 Immune IL2RA Hs.375596 Immune IL2RA Hs.75596 Immune IL2RA Hs.75596 Immune IL2RA Hs.75596 Immune IL2RA Hs.75596 Immune IL2RA Hs.172689 Immune IL2RA Hs.172689 Immune IL2RA Hs.172689 Immune IL2RA Hs.172689 Immune IL5RA Hs.68876 Immune IL5RA Hs.646 I	IL12RB1	Hs.121544 Immune	Cytokine/Chemokine Receptors	Both Databases
IL13RA2	IL12RB2	Hs.73165 Immune	Cytokine/Chemokine Receptors	
IL-15RA	IL13RA1	Hs.285115 Immune	Cytokine/Chemokine Receptors	EST
IL17BR	IL13RA2	Hs.25954 Immune	Cytokine/Chemokine Receptors	
IL-17RC	IL15RA	Hs.12503 Immune	Cytokine/Chemokine Receptors	. Microarray
IL-17RC Hs.129959 Immune IL-17RE Hs.31524 Immune IL-18R1 Hs.159301 Immune IL1R1 Hs.82112 Immune IL1R2 Hs.25333 Immune IL1RL1 Hs.66 Immune IL2RA Hs.21814 Immune IL2RA Hs.375184 Immune IL2RA Hs.172689 Immune IL2RA Hs.75596 Immune IL2RA Hs.75546 Immune IL5RA Hs.68876 Immune IL5RA Hs.68876 Immune IL5RA Hs.68876 Immune IL5RA Hs.193400 Immune IL5RA Hs.194778 Immune IL5RA Hs.194778 Immune IL5RA Hs.19478 Immune IL5RA Hs.1790 Immune IL5RA Hs.194778 Immune IL5Vokine/Chemokine Receptors IL5RA Hs.194778 Immune IL5RA Hs.1947	IL17BR	Hs.5470 Immune	Cytokine/Chemokine Receptors	
IL-17RE Hs.31524 Immune IL-18R1 Hs.159301 Immune IL-18R1 Hs.82112 Immune IL-18R1 Hs.25333 Immune IL-18R2 Hs.25333 Immune IL-18R2 Hs.102865 Immune IL-18R4 Hs.210546 Immune IL-20R4 Hs.21814 Immune IL-21R5 Hs.10915 Immune IL-22R64 Hs.110915 Immune IL-22R64 Hs.126891 Immune IL-23R6 Hs.386334 Immune IL-23R6 Hs.386334 Immune IL-28R6 Hs.386334 Immune IL-28R6 Hs.75596 Immune IL-28R6 Hs.75596 Immune IL-28R6 Hs.1724 Immune IL-28R6 Hs.172689 Immune IL-28R6 Hs.84 Immune IL-28R6 Hs.84 Immune IL-28R6 Hs.84 Immune IL-28R6 Hs.68876 Immune IL-28R6 Hs.68876 Immune IL-28R6 Hs.68876 Immune IL-28R6 Hs.68876 Immune IL-28R7 Hs.193400 Immune IL-28R8 Hs.193400 Immune IL-29R9 Hs.1702 Immune IN-29R9 Hs	IL17R	Hs.129751 Immune	Cytokine/Chemokine Receptors	
IL18R1	IL-17RC	Hs.129959 Immune	Cytokine/Chemokine Receptors	EST
IL18R1	IL-17RE	Hs.31524 Immune	Cytokine/Chemokine Receptors	
IL1R2		Hs.159301 Immune	Cytokine/Chemokine Receptors	
IL1RL1 Hs.66 Immune IL1RL2 Hs.102865 Immune IL2RA Hs.21814 Immune IL2RA Hs.110915 Immune IL2RA Hs.36831 Immune IL2RA Hs.386334 Immune IL2RA Hs.375184 Immune IL2RA Hs.175596 Immune IL2RB Hs.75596 Immune IL2RB Hs.75596 Immune IL2RB Hs.75545 Immune IL4R Hs.68876 Immune IL5RA Hs.193400 Immune IL5RA Hs.193400 Immune IL5RA Hs.193478 Immune IL5RA Hs.194778 Immune IL5RA Hs	IL1R1	Hs.82112 Immune	Cytokine/Chemokine Receptors	Microarray
IL1RL2 Hs.102865 Immune Cytokine/Chemokine Receptors IL20RA Hs.21814 Immune Cytokine/Chemokine Receptors IL21R Hs.210546 Immune Cytokine/Chemokine Receptors IL22R Hs.110915 Immune Cytokine/Chemokine Receptors IL22RA2 Hs.126891 Immune Cytokine/Chemokine Receptors IL23RA Hs.375184 Immune Cytokine/Chemokine Receptors IL28RA Hs.386334 Immune Cytokine/Chemokine Receptors IL28RA Hs.375596 Immune Cytokine/Chemokine Receptors IL2RB Hs.75596 Immune Cytokine/Chemokine Receptors IL2RG Hs.84 Immune Cytokine/Chemokine Receptors IL3RA Hs.172689 Immune Cytokine/Chemokine Receptors IL4R Hs.75545 Immune Cytokine/Chemokine Receptors IL5RA Hs.68876 Immune Cytokine/Chemokine Receptors IL5RA Hs.362807 Immune Cytokine/Chemokine Receptors IL5RA Hs.944778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors ILFR Hs.2798 Immune Cytokine/Chemokine Receptors ILTR Hs.2798 Immune Cytokine/Chemokine Receptors ILFR Hs.1116 Immune Cytokine/Chemokine Receptors ILTR Hs.2798 Immune Cytokine/Chemokine Receptors ILTR Hs.2798 Immune Cytokine/Chemokine Receptors ILTR Hs.2798 Immune Cytokine/Chemokine Receptors ILTR Hs.21827 Immune Cytokine/Chemokine Receptors INFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors INFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors INFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors INFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors I	IL1R2	Hs.25333 Immune	Cytokine/Chemokine Receptors	Both Databases
IL1RL2 Hs.102865 Immune Cytokine/Chemokine Receptors IL20RA Hs.21814 Immune Cytokine/Chemokine Receptors IL21R Hs.210546 Immune Cytokine/Chemokine Receptors IL22R Hs.110915 Immune Cytokine/Chemokine Receptors IL22RA Hs.126891 Immune Cytokine/Chemokine Receptors IL-23R Hs.375184 Immune Cytokine/Chemokine Receptors IL28RA Hs.386334 Immune Cytokine/Chemokine Receptors IL28RA Hs.1724 Immune Cytokine/Chemokine Receptors IL2RB Hs.75596 Immune Cytokine/Chemokine Receptors IL2RG Hs.84 Immune Cytokine/Chemokine Receptors IL3RA Hs.172689 Immune Cytokine/Chemokine Receptors IL4R Hs.75545 Immune Cytokine/Chemokine Receptors IL5RA Hs.68876 Immune Cytokine/Chemokine Receptors IL6R Hs.193400 Immune Cytokine/Chemokine Receptors IL8RA Hs.94778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL8RB Hs.1702 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors ILFR Hs.2798 Immune Cytokine/Chemokine Receptors ILFR Hs.1116 Immune Cytokine/Chemokine Receptors ILFR Hs.1827 Immune Cytokine/Chemokine Receptors INFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors INFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors INFRSF10D Hs.129844 Immune		Hs.66 Immune	Cytokine/Chemokine Receptors	
IL20RA		Hs.102865 immune	Cytokine/Chemokine Receptors	
IL21R		Hs.21814 Immune	Cytokine/Chemokine Receptors	
IL22R		Hs.210546 Immune	Cytokine/Chemokine Receptors	Microarray
IL22RA2 Hs.126891 Immune IL-23R Hs.375184 Immune IL28RA Hs.386334 Immune IL2RA Hs.1724 Immune IL2RB Hs.75596 Immune IL2RB Hs.75596 Immune IL2RG Hs.84 Immune IL3RA Hs.172689 Immune IL4R Hs.75545 Immune IL5RA Hs.93400 Immune IL6R Hs.193400 Immune IL7R Hs.362807 Immune IL8RA Hs.194778 Immune IL8RB Hs.1702 Immune IL8RB Hs.1702 Immune IL9R Hs.1702 Immune IL9R Hs.1702 Immune IL9R Hs.1703 Immune IL9R Hs.1827 Immune ILFR Hs.2798 Immune ILFR Hs.1827 Immune INFRSF10B Hs.51233 Immune INFRSF10C Hs.119684 Immune IL5RA Hs.19844 Immune IL5RA Hs.119684 Immune IL5RA Hs.119	IL22R	Hs.110915 Immune	Cytokine/Chemokine Receptors	
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IL28RAHs.386334 ImmuneCytokine/Chemokine ReceptorsIL2RAHs.1724 ImmuneCytokine/Chemokine ReceptorsESTIL2RBHs.75596 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesIL2RGHs.84 ImmuneCytokine/Chemokine ReceptorsESTIL3RAHs.172689 ImmuneCytokine/Chemokine ReceptorsESTIL4RHs.75545 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesIL5RAHs.68876 ImmuneCytokine/Chemokine ReceptorsMicroarrayIL6RHs.193400 ImmuneCytokine/Chemokine ReceptorsESTIL7RHs.362807 ImmuneCytokine/Chemokine ReceptorsESTIL8RAHs.194778 ImmuneCytokine/Chemokine ReceptorsESTIL8RBHs.846 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesIL9RHs.1702 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesLIFRHs.2798 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesLTBRHs.1116 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesNGFRHs.1827 ImmuneCytokine/Chemokine ReceptorsMicroarrayTNFRSF10AHs.249190 ImmuneCytokine/Chemokine ReceptorsMicroarrayTNFRSF10BHs.51233 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesTNFRSF10DHs.119684 ImmuneCytokine/Chemokine ReceptorsBoth DatabasesTNFRSF10DHs.129844 ImmuneCytokine/Chemokine ReceptorsBoth Databases		Hs.375184 Immune	Cytokine/Chemokine Receptors	
IL2RB Hs.75596 Immune Cytokine/Chemokine Receptors IL2RG Hs.84 Immune Cytokine/Chemokine Receptors IL3RA Hs.172689 Immune Cytokine/Chemokine Receptors IL4R Hs.75545 Immune Cytokine/Chemokine Receptors IL5RA Hs.68876 Immune Cytokine/Chemokine Receptors IL6R Hs.193400 Immune Cytokine/Chemokine Receptors IL7R Hs.362807 Immune Cytokine/Chemokine Receptors IL8RA Hs.194778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors ILFR Hs.2798 Immune Cytokine/Chemokine Receptors LIFR Hs.1116 Immune Cytokine/Chemokine Receptors LTBR Hs.1116 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Recept		Hs.386334 Immune	Cytokine/Chemokine Receptors	
IL2RB Hs.75596 Immune IL2RG Hs.84 Immune IL3RA Hs.172689 Immune IL3RA Hs.75545 Immune IL4R Hs.75545 Immune IL5RA Hs.68876 Immune IL6R Hs.193400 Immune IL7R Hs.362807 Immune IL8RA Hs.194778 Immune IL8RB Hs.846 Immune IL9R Hs.1702 Immune IL9R Hs.1702 Immune ILFR Hs.2798 Immune ILFR Hs.2798 Immune ILFR Hs.1116 Immune ILFR Hs.1827 Immune ITFRSF10A Hs.249190 Immune INFRSF10B Hs.51233 Immune INFRSF10C Hs.119684 Immune IL2RB IL3RA Immune IL5RA Hs.119684 Immune IL5RA Hs.129844 Immune IL5RA Hs.119684 Immune IL5RA Hs.119684 Immune IL5RA Hs.119684 Immune IL5RA Hs.129844 Immune IL5RA Hs.119684 Immune IL5RA Hs.119484 Immune I		Hs.1724 Immune	Cytokine/Chemokine Receptors	EST
IL2RG Hs.84 Immune Cytokine/Chemokine Receptors IL3RA Hs.172689 Immune Cytokine/Chemokine Receptors IL4R Hs.75545 Immune Cytokine/Chemokine Receptors IL5RA Hs.68876 Immune Cytokine/Chemokine Receptors IL6R Hs.193400 Immune Cytokine/Chemokine Receptors IL7R Hs.362807 Immune Cytokine/Chemokine Receptors IL8RA Hs.194778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors ILFR Hs.2798 Immune Cytokine/Chemokine Receptors ILTBR Hs.1116 Immune Cytokine/Chemokine Receptors ILTBR Hs.1116 Immune Cytokine/Chemokine Receptors INFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors Cytok		Hs.75596 Immune	Cytokine/Chemokine Receptors	Both Databases
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IL4R Hs.75545 Immune Cytokine/Chemokine Receptors IL5RA Hs.68876 Immune Cytokine/Chemokine Receptors IL6R Hs.193400 Immune Cytokine/Chemokine Receptors IL7R Hs.362807 Immune Cytokine/Chemokine Receptors IL8RA Hs.194778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors ILFR Hs.2798 Immune Cytokine/Chemokine Receptors ILTBR Hs.1116 Immune Cytokine/Chemokine Receptors INFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors	IL3RA	Hs.172689 Immune	Cytokine/Chemokine Receptors	EST
IL5RA Hs.68876 Immune Cytokine/Chemokine Receptors IL6R Hs.193400 Immune Cytokine/Chemokine Receptors IL7R Hs.362807 Immune Cytokine/Chemokine Receptors IL8RA Hs.194778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors ILFR Hs.2798 Immune Cytokine/Chemokine Receptors ILTBR Hs.1116 Immune Cytokine/Chemokine Receptors ILTBR Hs.1827 Immune Cytokine/Chemokine Receptors INFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors INFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors INFRSF10D Hs.119684 Immune Cytokine/Chemokine Receptors INFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors INFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors INFRSF10D Cytokine/Chemokine Receptors INFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors INFRSF10D C			Cytokine/Chemokine Receptors	Both Databases
IL6R Hs.193400 Immune Cytokine/Chemokine Receptors IL7R Hs.362807 Immune Cytokine/Chemokine Receptors IL8RA Hs.194778 Immune Cytokine/Chemokine Receptors IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors LIFR Hs.2798 Immune Cytokine/Chemokine Receptors LTBR Hs.1116 Immune Cytokine/Chemokine Receptors NGFR Hs.1827 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors		Hs.68876 Immune	Cytokine/Chemokine Receptors	Microarray
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IL8RA Hs.194778 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors LIFR Hs.2798 Immune Cytokine/Chemokine Receptors LTBR Hs.1116 Immune Cytokine/Chemokine Receptors NGFR Hs.1827 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors		Hs.362807 Immune	Cytokine/Chemokine Receptors	EST
IL8RB Hs.846 Immune Cytokine/Chemokine Receptors IL9R Hs.1702 Immune Cytokine/Chemokine Receptors LIFR Hs.2798 Immune Cytokine/Chemokine Receptors LTBR Hs.1116 Immune Cytokine/Chemokine Receptors NGFR Hs.1827 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors			•	Both Databases
IL9R Hs.1702 Immune Cytokine/Chemokine Receptors LIFR Hs.2798 Immune Cytokine/Chemokine Receptors LTBR Hs.1116 Immune Cytokine/Chemokine Receptors NGFR Hs.1827 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors			Cytokine/Chemokine Receptors	
LIFR Hs.2798 Immune Cytokine/Chemokine Receptors LTBR Hs.1116 Immune Cytokine/Chemokine Receptors NGFR Hs.1827 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors			Cytokine/Chemokine Receptors	
LTBR Hs.1116 Immune Cytokine/Chemokine Receptors NGFR Hs.1827 Immune Cytokine/Chemokine Receptors TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors Cytokine/Chemokine Receptors			Cytokine/Chemokine Receptors	
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TNFRSF10A Hs.249190 Immune Cytokine/Chemokine Receptors Microarray TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors			Cytokine/Chemokine Receptors	Microarray
TNFRSF10B Hs.51233 Immune Cytokine/Chemokine Receptors Both Databases TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors			•	Microarray
TNFRSF10C Hs.119684 Immune Cytokine/Chemokine Receptors TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors				Both Databases
TNFRSF10D Hs.129844 Immune Cytokine/Chemokine Receptors				
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TNFRSF11B	Hs.81791 Immune	Cytokine/Chemokine Receptors	
	Hs.158341 Immune	Cytokine/Chemokine Receptors	Both Databases
TNFRSF13C	Hs.344088 Immune	Cytokine/Chemokine Receptors	
TNFRSF14	Hs.279899 Immune	Cytokine/Chemokine Receptors	Both Databases
TNFRSF17	Hs.2556 Immune	Cytokine/Chemokine Receptors	
TNFRSF18	Hs.212680 Immune	Cytokine/Chemokine Receptors	EST
TNFRSF19	Hs.283615 Immune	Cytokine/Chemokine Receptors	
TNFRSF19L	Hs.79707 Immune	Cytokine/Chemokine Receptors	EST
TNFRSF1A	Hs.159 Immune	Cytokine/Chemokine Receptors	Microarray
TNFRSF1B	Hs.256278 Immune	Cytokine/Chemokine Receptors	Both Databases
TNFRSF21	Hs.159651 Immune	Cytokine/Chemokine Receptors	Microarray
TNFRSF25	Hs.180338 Immune	Cytokine/Chemokine Receptors	Both Databases
TNFRSF4	Hs.129780 Immune	Cytokine/Chemokine Receptors	Both Databases
TNFRSF5	Hs.25648 Immune	Cytokine/Chemokine Receptors	Both Databases
TNFRSF6	Hs.82359 Immune	Cytokine/Chemokine Receptors	EST
TNFRSF6B	Hs.348183 Immune	Cytokine/Chemokine Receptors	Microarray
TNFRSF7	Hs.355307 Immune	Cytokine/Chemokine Receptors	EST
TNFRSF8	Hs.1314 Immune	Cytokine/Chemokine Receptors	EST
WSX1	Hs.132781 Immune	Cytokine/Chemokine Receptors	EST
XCR1	Hs.248116 Immune	Cytokine/Chemokine Receptors	Microarray
CCL1	Hs.72918 Immune	Cytokines/Chemokines	
CCL11	Hs.54460 Immune	Cytokines/Chemokines	Microarray
CCL13	Hs.11383 Immune	Cytokines/Chemokines	
CCL14	Hs.20144 Immune	Cytokines/Chemokines	Microarray
CCL15	Hs.272493 Immune	Cytokines/Chemokines	Microarray
CCL16	Hs.10458 Immune	Cytokines/Chemokines	Microarray
CCL17	Hs.66742 Immune	Cytokines/Chemokines	Microarray
CCL18	Hs.16530 Immune	Cytokines/Chemokines	Microarray
CCL19	Hs.50002 Immune	Cytokines/Chemokines	Microarray
CCL2	Hs.303649 Immune	Cytokines/Chemokines	EST
CCL20	Hs.75498 Immune	Cytokines/Chemokines	Microarray
CCL21	Hs.57907 Immune	Cytokines/Chemokines	Microarray
CCL22	Hs.97203 Immune	Cytokines/Chemokines	EST
CCL23	Hs.169191 Immune	Cytokines/Chemokines	
CCL24	Hs.247838 Immune	Cytokines/Chemokines	Microarray
CCL25	Hs.50404 Immune	Cytokines/Chemokines	Microarray
CCL26	Hs.131342 Immune	Cytokines/Chemokines	
CCL27	Hs.225948 Immune	Cytokines/Chemokines	Microarray
CCL28	Hs.283090 Immune	Cytokines/Chemokines	Microarray
CCL4	Hs.75703 Immune	Cytokines/Chemokines	Both Databases
CCL5	Hs.241392 Immune	Cytokines/Chemokines	Both Databases
CCL7	Hs.251526 Immune	Cytokines/Chemokines	B 4'
CCL8	Hs.271387 Immune	Cytokines/Chemokines	Microarray
CSF1	Hs.173894 Immune	Cytokines/Chemokines	EST
CSF2	Hs.1349 Immune	Cytokines/Chemokines	EST
CSF3	Hs.2233 Immune	Cytokines/Chemokines	Microarray
CTF1	Hs.25537 Immune	Cytokines/Chemokines	Microarray
CX3CL1	Hs.80420 Immune	Cytokines/Chemokines	Microarray
CXCL1	Hs.789 Immune	Cytokines/Chemokines	Microarray
CXCL10	Hs.2248 Immune	Cytokines/Chemokines	EST

	,		
CXCL11	Hs.103982 Immune	Cytokines/Chemokines	
CXCL12	Hs.237356 Immune	Cytokines/Chemokines	Microarray
CXCL13	Hs.100431 Immune	Cytokines/Chemokines	
CXCL14	Hs.24395 Immune	Cytokines/Chemokines	
CXCL16	Hs.82407 Immune	Cytokines/Chemokines	
CXCL2	Hs.75765 Immune	Cytokines/Chemokines	Both Databases
CXCL3	Hs.89690 Immune	Cytokines/Chemokines	Both Databases
CXCL5	Hs.89714 Immune	Cytokines/Chemokines	Microarray
CXCL6	Hs.164021 Immune	Cytokines/Chemokines	
CXCL9	Hs.77367 Immune	Cytokines/Chemokines	EST
IL10	Hs.193717 Immune	Cytokines/Chemokines	Both Databases
IL11	Hs.1721 Immune	Cytokines/Chemokines	
IL12A	Hs.673 Immune	Cytokines/Chemokines	
IL12B	Hs.674 Immune	Cytokines/Chemokines	Microarray
IL13	Hs.845 Immune	Cytokines/Chemokines	
IL14	Hs.406680 Immune	Cytokines/Chemokines	
IL15	Hs.168132 Immune	Cytokines/Chemokines	
IL16	Hs.82127 Immune	Cytokines/Chemokines	EST
IL17	Hs.41724 Immune	Cytokines/Chemokines	Microarray
IL17B	Hs.110040 Immune	Cytokines/Chemokines	Microarray
IL17C	Hs.278911 Immune	Cytokines/Chemokines	Microarray
IL17D	Hs.32450 Immune	Cytokines/Chemokines	EST
IL17E	Hs.302036 Immune	Cytokines/Chemokines	Microarray
IL17F	Hs.272295 Immune	Cytokines/Chemokines	·
IL18 .	Hs.83077 Immune	Cytokines/Chemokines	Microarray
IL19	Hs.71979 Immune	Cytokines/Chemokines	Microarray
IL1A	Hs.1722 Immune	Cytokines/Chemokines	Microarray
IL1B	Hs.126256 Immune	Cytokines/Chemokines	Both Databases
IL1F10	Hs.306974 Immune	Cytokines/Chemokines	
IL1F5	Hs.207224 Immune	Cytokines/Chemokines	Microarray
IL1F6	Hs.278910 Immune	Cytokines/Chemokines	Microarray
IL1F7	Hs.166371 Immune	Cytokines/Chemokines	
IL1F8	Hs.278909 Immune	Cytokines/Chemokines	
IL1F9	Hs.211238 Immune	Cytokines/Chemokines	
IL2	Hs.89679 Immune	Cytokines/Chemokines	
IL20	Hs.272373 Immune	Cytokines/Chemokines	Microarray
IL21	Hs.302014 Immune	Cytokines/Chemokines	
IL22	Hs.287369 Immune	Cytokines/Chemokines	Microarray
IL23A	Hs.98309 Immune	Cytokines/Chemokines	EST
IL24	Hs.315463 Immune	Cytokines/Chemokines	Microarray
IL26	Hs.272350 Immune	Cytokines/Chemokines	Microarray
IL27w	Hs.10927 Immune	Cytokines/Chemokines	EST
IL3	Hs.694 Immune	Cytokines/Chemokines	Microarray
IL4	Hs.73917 Immune	Cytokines/Chemokines	Both Databases
IL5	Hs.2247 Immune	Cytokines/Chemokines	Microarray
IL6	Hs.93913 Immune	Cytokines/Chemokines	Microarray
IL7	Hs.72927 Immune	Cytokines/Chemokines	EST
IL8	Hs.624 Immune	Cytokines/Chemokines	EST
IL9	Hs.960 Immune	Cytokines/Chemokines	
LIF	Hs.2250 Immune	Cytokines/Chemokines	Microarray

LTA Hs.36 Immune Cytokines/Chemokines Microarray MIF Hs.73798 Immune Cytokines/Chemokines EST N-PAC Hs.374985 Immune Cytokines/Chemokines	
Will Florida Hillians Systemics Charles	
N-PAC Hs.374985 Immune Cytokines/Chemokines	
OSM Hs.248156 Immune Cytokines/Chemokines Both Database	es
OSMR Hs.238648 Immune Cytokines/Chemokines Microarray	
PF4 Hs.81564 Immune Cytokines/Chemokines	
PLAB Hs.296638 Immune Cytokines/Chemokines EST	
PPBP Hs.2164 Immune Cytokines/Chemokines Both Database	
SCYA3 Hs.73817 Immune Cytokines/Chemokines Both Database	es
SCYE1 Hs.333513 Immune Cytokines/Chemokines EST	
TNF Hs.241570 Immune Cytokines/Chemokines Both Database	es
TNFRSF9 Hs.73895 Immune Cytokines/Chemokines EST	
TNFSF10 Hs.83429 Immune Cytokines/Chemokines	
TNFSF11 Hs.115770 Immune Cytokines/Chemokines	
TNFSF12 Hs.26401 Immune Cytokines/Chemokines EST	
TNFSF13 Hs.54673 Immune Cytokines/Chemokines Both Databas	
TNFSF13B Hs.270737 Immune Cytokines/Chemokines Both Databas	es
TNFSF14 Hs.129708 Immune Cytokines/Chemokines Microarray	
TNFSF15 Hs.241382 Immune Cytokines/Chemokines	
TNFSF18 Hs.248197 Immune Cytokines/Chemokines	
TNFSF4 Hs.181097 Immune Cytokines/Chemokines	
TNFSF5 Hs.652 Immune Cytokines/Chemokines Microarray	
TNFSF7 Hs.99899 Immune Cytokines/Chemokines Microarray	
TNFSF8 Hs.1313 Immune Cytokines/Chemokines	
TNFSF9 Hs.1524 Immune Cytokines/Chemokines Microarray	
XCL1 Hs.3195 Immune Cytokines/Chemokines	
XCL2 Hs.174228 Immune Cytokines/Chemokines	
YARS Hs.239307 Immune Cytokines/Chemokines EST	
BAT1 Hs.55296 Immune Immune: MHC/HLA Both Databas	es.
HLA-A Hs.181244 Immune Immune: MHC/HLA EST	
HLA-B Hs.77961 Immune Immune: MHC/HLA EST	
HLA-C Hs.277477 Immune Immune: MHC/HLA EST	
HLA-DNA Hs.351874 Immune Immune: MHC/HLA Microarray	
HLA-DPA1 Hs.914 Immune Immune: MHC/HLA EST	
HLA-DPB1 Hs.814 Immune Immune: MHC/HLA EST	
HLA-DQA1 Hs.198253 Immune Immune: MHC/HLA EST	
HLA-DQB1 Hs.73931 Immune Immune: MHC/HLA EST	
HLA-DRA Hs.76807 Immune Immune: MHC/HLA EST	
HLA-DRB3 Hs.308026 Immune Immune: MHC/HLA EST	
HLA-DRB4 Hs.318720 Immune Immune: MHC/HLA EST	
HLA-DRB5 Hs.352392 Immune Immune: MHC/HLA EST	
HLA-E Hs.381008 Immune Immune: MHC/HLA EST	
LILRB4 Hs.67846 Immune Immune: MHC/HLA EST	
MHC2TA Hs.3076 Immune Immune: MHC/HLA EST	
MICA Hs.90598 Immune Immune: MHC/HLA EST	
NSEP1 Hs.74497 Immune Immune: MHC/HLA EST	
PSMB8 Hs.180062 Immune Immune: MHC/HLA Both Databas	es
PSMB9 Hs.381081 Immune Immune: MHC/HLA EST	
RFXANK Hs.296776 Immune Immune: MHC/HLA Both Databas	es
RFXAP Hs.24422 Immune Immune: MHC/HLA	

ABCÀ7	Hs.134514 Immune	Other Immune Function	
ADA	Hs.1217 Immune	Other Immune Function	EST
ADAM8	Hs.86947 Immune	Other Immune Function	Both Databases
ADAR	Hs.7957 Immune	Other Immune Function	EST
ADIR	Hs.26267 Immune	Other Immune Function	Both Databases
ADORA1	Hs.77867 Immune	Other Immune Function	Microarray
ADORA2A	Hs.1613 Immune	Other Immune Function	Microarray
AIM2	Hs.105115 Immune	Other Immune Function	EST
ALOX12B	Hs.136574 Immune	Other Immune Function	
ALOX5	Hs.89499 Immune	Other Immune Function	EST
ALOX5AP	Hs.100194 Immune	Other Immune Function	Both Databases
ANXA1	Hs.78225 Immune	Other Immune Function	EST
ANXA11	Hs.75510 Immune	Other Immune Function	EST
ANXA13	Hs.181107 Immune	Other Immune Function	
ANXA2	Hs.217493 Immune	Other Immune Function	Both Databases
ANXA3	Hs.1378 Immune	Other Immune Function	
ANXA4	Hs.77840 Immune	Other Immune Function	EST
ANXA5	Hs.300711 Immune	Other Immune Function	EST
ANXA6	Hs.118796 Immune	Other Immune Function	EST
ANXA7	Hs.386741 Immune	Other Immune Function	EST
ANXA8	Hs.87268 Immune	Other Immune Function	Microarray
APOE	Hs.169401 Immune	Other Immune Function	Microarray
B2M	Hs.48516 Immune	Other Immune Function	EST
B7H2	Hs.14155 Immune	Other Immune Function	EST
B7-H3	Hs.77873 Immune	Other Immune Function	Microarray
BSG	Hs.74631 Immune	Other Immune Function	Both Databases
BTK	Hs.159494 Immune	Other Immune Function	EST
CANX	Hs.155560 Immune	Other Immune Function	EST
CAST	Hs.359682 Immune	Other Immune Function	EST
CD19	Hs.96023 Immune	Other Immune Function	
CD1A	Hs.1309 Immune	Other Immune Function	
CD1A CD1B	Hs.1310 Immune	Other Immune Function	Microarray
CD1B CD1C	Hs.1311 Immune	Other Immune Function	morourray
CD1C	Hs.1799 Immune	Other Immune Function	
CD1E	Hs.249217 Immune	Other Immune Function	
CD1E	Hs.89476 Immune	Other Immune Function	Both Databases
CD209	Hs.278694 Immune	Other Immune Function	Microarray
CD209 CD209L	Hs.23759 Immune	Other Immune Function	Microarray
		Other Immune Function	Both Databases
CD28		Other Immune Function	Both Batabacce
CD34	Hs.374990 Immune Hs.66052 Immune	Other Immune Function	Microarray
CD38		Other Immune Function	EST
CD3D	Hs.95327 Immune	Other Immune Function	EST
CD3E	Hs.3003 Immune	Other Immune Function	
CD3G	Hs.2259 Immune	Other Immune Function	EST
CD3Z	Hs.97087 Immune	Other Immune Function	
CD4	Hs.17483 Immune	Other Immune Function	EST
CD44	Hs.169610 Immune	Other Immune Function	Both Databases
CD5	Hs.58685 Immune	Other Immune Function	Microarray
CD58	Hs.75626 Immune		Both Databases
CD69	Hs.82401 Immune	Other Immune Function	องเบ บลเสมสรศร

CD74	Hs.84298 Immune	Other Immune Function	Both Databases
CD80	Hs.838 Immune	Other Immune Function	
CD81	Hs.54457 Immune	Other Immune Function	EST
CD84	Hs.137548 Immune	Other Immune Function	Microarray
CD86	Hs.27954 Immune	Other Immune Function	Both Databases
CD8A	Hs.85258 Immune	Other Immune Function	EST
CD8B1	Hs.2299 Immune	Other Immune Function	EST
CDR2	Hs.75124 Immune	Other Immune Function	EST
CIAS1	Hs.159483 Immune	Other Immune Function	Microarray
CLC	Hs.132004 Immune	Other Immune Function	Both Databases
CML66	Hs.195870 Immune	Other Immune Function	
CNIH	Hs.201673 Immune	Other Immune Function	Microarray
CTLA4	Hs.247824 Immune	Other Immune Function	Both Databases
CTSB	Hs.297939 Immune	Other Immune Function	Microarray
CTSC	Hs.10029 Immune	Other Immune Function	EST
CTSD	Hs.343475 Immune	Other Immune Function	Both Databases
CTSW	Hs.87450 Immune	Other Immune Function	Both Databases
CYSLTR1	Hs.124401 Immune	Other Immune Function	;
CYSLTR2	Hs.253706 Immune	Other Immune Function	
DCNP1	Hs.143271 Immune	Other Immune Function	
DEFA4	Hs.2582 Immune	Other Immune Function	
EAF1	Hs.350352 Immune	Other Immune Function	
EAT2	Hs.350581 Immune	Other Immune Function	EST
EBI3	Hs.185705 Immune	Other Immune Function	
ED1	Hs.105407 Immune	Other Immune Function	Microarray
FCER1A	Hs.897 Immune	Other Immune Function	whoroarray
FCER1G	Hs.433300 Immune	Other Immune Function	EST
FCER2	Hs.1416 Immune	Other Immune Function	Both Databases
FCGBP	Hs.111732 Immune	Other Immune Function	Microarray
FCGR1A	Hs.77424 Immune	Other Immune Function	EST
FCGR2A	Hs.78864 Immune	Other Immune Function	Microarray
FCGR2B	Hs.278443 Immune	Other Immune Function	Both Databases
FCGR3A	Hs.176663 Immune	Other Immune Function	EST
FCGR3B	Hs.372679 Immune	Other Immune Function	LOT
FCGRT	Hs.111903 Immune	Other Immune Function	Both Databases
FETUB	Hs.81073 Immune	Other Immune Function	Microarray
FKBP1A	Hs.374638 Immune	Other Immune Function	
FKBP1B	Hs.77643 Immune	Other Immune Function	
FKBP2	Hs.227729 Immune	Other Immune Function	
FKBP3	Hs.379557 Immune	Other Immune Function	Dath Databases
FKBP5	Hs.7557 Immune	Other Immune Function	Both Databases
FKBP6	Hs.150490 Immune	Other Immune Function	FOT
FKBP8	Hs.173464 Immune	Other Immune Function	EST
FPR1	Hs.753 Immune	Other Immune Function	EST
FUS	Hs.99969 Immune	Other Immune Function	Both Databases
G1P2	Hs.432233 Immune	Other Immune Function	EST
G1P3	Hs.265827 Immune	Other Immune Function	Both Databases
GBP1	Hs.62661 Immune	Other Immune Function	EST
GBP4	Hs.240849 Immune	Other Immune Function	EST
GBP5	Hs.237809 Immune	Other Immune Function	EST

GGTLA1	Hs.1675 Immune	Other Immune Function	Microarray
GPS2	Hs.438219 Immune	Other Immune Function	
GZMB	Hs.1051 Immune	Other Immune Function	Both Databases
GZMM	Hs.268531 Immune	Other Immune Function	Microarray
HAL	Hs.276590 Immune	Other Immune Function	
HAVCR2	Hs.155111 Immune	Other Immune Function	EST
HDC	Hs.1481 Immune	Other Immune Function	Microarray
HLA-DRB1	Hs.375570 Immune	Other Immune Function	EST
HLALS	Hs.101840 Immune	Other Immune Function	Microarray
HRH1	Hs.1570 Immune	Other Immune Function	
HRH2	Hs.247885 Immune	Other Immune Function	Microarray
HRH4	Hs.287388 Immune	Other Immune Function	
IAN4L1	Hs.26194 Immune	Other Immune Function	EST
ICAM1	Hs.168383 Immune	Other Immune Function	Both Databases
ICAM2	Hs.433303 Immune	Other Immune Function	EST
ICAM3	Hs.99995 Immune	Other Immune Function	Both Databases
ICAM4	Hs.108287 Immune	Other Immune Function	Microarray
ICAM5	Hs.151250 Immune	Other Immune Function	Microarray
ICOS	Hs.56247 Immune	Other Immune Function	EST
IFI16	Hs.155530 Immune	Other Immune Function	EST
IFI27	Hs.278613 Immune	Other Immune Function	Both Databases
IFI30	Hs.14623 Immune	Other Immune Function	EST
IFI35	Hs.50842 Immune	Other Immune Function	EST
IF144	Hs.82316 Immune	Other Immune Function	Microarray
IFIT1	Hs.20315 Immune	Other Immune Function	Microarray
IFIT2	Hs.169274 Immune	Other Immune Function	1
IFIT4	Hs.181874 Immune	Other Immune Function	Both Databases
IFITM1	Hs.366 Immune	Other Immune Function	EST
IFITM2	Hs.174195 Immune	Other Immune Function	EST
IFITM3	Hs.433414 Immune	Other Immune Function	EST
IFNA1	Hs.37026 Immune	Other Immune Function	
IFNA10	Hs.282275 Immune	Other Immune Function	
IFNA14	Hs.93907 Immune	Other Immune Function	
IFNA16	Hs.56303 Immune	Other Immune Function	
IFNA17	Hs.282276 Immune	Other Immune Function	
IFNA2	Hs.211575 Immune	Other Immune Function	
IFNA21	Hs.113211 Immune	Other Immune Function	
IFNA4	Hs.1510 Immune	Other Immune Function	
IFNA5	Hs.37113 Immune	Other Immune Function	
IFNA6	Hs.247933 Immune	Other Immune Function	
IFNA7	Hs.282274 Immune	Other Immune Function	
IFNA8	Hs.73890 Immune	Other Immune Function	Microarray
IFNAR1	Hs.1513 Immune	Other Immune Function	
IFNAR2	Hs.86958 Immune	Other Immune Function	EST
IFNB1	Hs.93177 Immune	Other Immune Function	
IFNG	Hs.856 Immune	Other Immune Function	Both Databases
IFNGR1	Hs.180866 Immune	Other Immune Function	EST
IFNGR2	Hs.177559 Immune	Other Immune Function	EST
IFNK	Hs.283810 Immune	Other Immune Function	
IFNW1 \	Hs.73010 Immune	Other Immune Function	Microarray

IFRD1	Hs.7879 Immune	Other Immune Function	Microarray
IFRD2	Hs.315177 Immune	Other Immune Function	Both Databases
IKBKAP	Hs.31323 Immune	Other Immune Function	Microarray
IKBKB	Hs.226573 Immune	Other Immune Function	EST
IKBKE	Hs.321045 Immune	Other Immune Function	Microarray
IKBKG	Hs.43505 Immune	Other Immune Function	Both Databases
INDO	Hs.840 Immune	Other Immune Function	
IRF4	Hs.82132 Immune	Other Immune Function	EST
ITGA1	Hs.116774 Immune	Other Immune Function	
ITGA2	Hs.271986 Immune	Other Immune Function	Both Databases
ITGA3	Hs.265829 Immune	Other Immune Function	Both Databases
ITGA4	Hs.40034 Immune	Other Immune Function	EST
ITGA5	Hs.149609 Immune	Other Immune Function	EST
ITGA6	Hs.227730 Immune	Other Immune Function	
ITGAL	Hs.174103 Immune	Other Immune Function	Both Databases
ITGAX	Hs.51077 Immune	Other Immune Function	EST
JAM2	Hs.54650 Immune	Other Immune Function	
JIK	Hs.12040 Immune	Other Immune Function	Microarray
KIR2DS2	Hs.74134 Immune	Other Immune Function	EST
KLRB1	Hs.169824 Immune	Other Immune Function	EST
KLRD1	Hs.41682 Immune	Other Immune Function	EST
KPNB2	Hs.168075 Immune	Other Immune Function	EST
LAIR1	Hs.115808 Immune	Other Immune Function	EST
LAIR2	Hs.43803 Immune	Other Immune Function	, 13.
LAT	Hs.83496 Immune	Other Immune Function	Both Databases
LBP	Hs.154078 Immune	Other Immune Function	Microarray
LCP1	Hs.381099 Immune	Other Immune Function	EST
LGALS3BP	Hs.79339 Immune	Other Immune Function	Both Databases
LOC284057	Hs.380993 Immune	Other Immune Function	Don Databases
LRBA	Hs.62354 Immune	Other Immune Function	
LST1	Hs.380427 Immune	Other Immune Function	EST
LTA4H	Hs.81118 Immune	Other Immune Function	Microarray
LTB	Hs.890 Immune	Other Immune Function	Both Databases
LTB4R	Hs.28408 Immune	Other Immune Function	Both Databases
LTB4R2	Hs.130685 Immune	Other Immune Function	Both Databases
LTC4S	Hs.456 Immune	Other Immune Function	Microarray
MBP	Hs.69547 Immune	Other Immune Function	EST
MD-2	Hs.69328 Immune	Other Immune Function	231
MGST2	Hs.81874 Immune	Other Immune Function	Microarray
MGST2	Hs.111811 Immune	Other Immune Function	EST
MICB	Hs.211580 Immune	Other Immune Function	EST
MIG-6	Hs.11169 Immune	Other Immune Function	
MMP1		Other Immune Function	Microarray
MMP2	Hs.83169 Immune Hs.111301 Immune	Other Immune Function	Microarray
MMP25		Other Immune Function	iviidioaitay
MMP3	Hs.198265 Immune	Other Immune Function Other Immune Function	
	Hs.83326 Immune		
MMP8	Hs.73862 Immune	Other Immune Function	Microcress
MMP9 MPL	Hs.151738 Immune	Other Immune Function Other Immune Function	Microarray
	Hs.84171 Immune		Microarray
MST1R	Hs.2942 Immune	Other Immune Function	Microarray

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MX1	Hs.76391 Immune	Other Immune Function	Both Databases
MX2	Hs.926 Immune	Other Immune Function	
NCAM1	Hs.167988 Immune	Other Immune Function	Both Databases
NCR3	Hs.88411 Immune	Other Immune Function	EST
NFATC1	Hs.96149 Immune	Other Immune Function	Microarray
NFIL3	Hs.79334 Immune	Other Immune Function	Microarray
NP	Hs.75514 Immune	Other Immune Function	EST
NYREN18	Hs.279780 Immune	Other Immune Function	EST
OAS1	Hs.442936 Immune	Other Immune Function	
OAS2	Hs.414332 Immune	Other Immune Function	
PADI5	Hs.117232 Immune	Other Immune Function	Both Databases
PAK1	Hs.64056 Immune	Other Immune Function	EST
PECAM1	Hs.78146 Immune	Other Immune Function	EST
PGDS	Hs.128433 Immune	Other Immune Function	Microarray
PIGR	Hs.205126 Immune	Other Immune Function	•
PIK3CG	Hs.32942 Immune	Other Immune Function	Both Databases
PILR(ALPHA) Hs.122591 Immune	Other Immune Function	Both Databases
PILR(BETA)	Hs.349256 Immune	Other Immune Function	Both Databases
PLA2G2E	Hs.272372 Immune	Other Immune Function	Microarray
PLA2G4A	Hs.211587 Immune	Other Immune Function	moroarray
PLA2G6	Hs.120360 Immune	Other Immune Function	
PLA2R1	Hs.171945 Immune	Other Immune Function	
PPARD	Hs.106415 Immune	Other Immune Function	Both Databases
PPIA	Hs.401787 Immune	Other Immune Function	EST
PRKRIR	Hs.177574 Immune	Other Immune Function	LOT
PRV1	Hs.232165 Immune	Other Immune Function	Microarray
PTCRA	Hs.169002 Immune	Other Immune Function	Microarray
PTGDR	Hs.158326 Immune	Other Immune Function	Microarray
PTGDS	Hs.8272 Immune	Other Immune Function	EST
PTGER1	Hs.159360 Immune	Other Immune Function	Microarray
PTGER2	Hs.2090 Immune	Other Immune Function	Microarray
PTGER3	Hs.170917 Immune	Other Immune Function	Microarray
PTGER4	Hs.199248 Immune	Other Immune Function	
PTGES	Hs.146688 Immune	Other Immune Function	
PTGES2			Both Databases
	Hs.288102 Immune	Other Immune Function	
PTGFR	Hs.89418 Immune	Other Immune Function	Microarray
PTGIR	Hs.393 Immune	Other Immune Function	EST
PTGS1 PTGS2	Hs.88474 Immune	Other Immune Function	Both Databases
	Hs.196384 Immune	Other Immune Function	Both Databases
PTPN22	Hs.87860 Immune	Other Immune Function	Microarray
PTPN7	Hs.35 Immune	Other Immune Function	EST
PTPN9	Hs.147663 Immune	Other Immune Function	EST
PTPRC	Hs.170121 Immune	Other Immune Function	Both Databases
PTPRK	Hs.79005 Immune	Other Immune Function	D-#- D / 1
RAG1	Hs.73958 Immune	Other Immune Function	Both Databases
RAG2	Hs.159376 Immune	Other Immune Function	
RAI	Hs.324051 Immune	Other Immune Function	Microarray
RelA	Hs.75569 Immune	Other Immune Function	EST
RELB	Hs.858 Immune	Other Immune Function	Both Databases
RFC1	Hs.166563 Immune	Other Immune Function	EST

RI58	Hs.27610 Immune	Other Immune Function	
RNASE3	Hs.73839 Immune	Other Immune Function	Microarray
SAMHD1	Hs.23889 Immune	Other Immune Function	Both Databases
SECTM1	Hs.95655 Immune	Other Immune Function	EST
SELE	Hs.89546 Immune	Other Immune Function	
SELL	Hs.82848 Immune	Other Immune Function	Both Databases
SELPLG	Hs.79283 Immune	Other Immune Function	EST
SEMA4D	Hs.79089 Immune	Other Immune Function	EST
SIGLEC5	Hs.117005 Immune	Other Immune Function	Both Databases
SLAM	Hs.32970 Immune	Other Immune Function	EST
SLC21A2	Hs.83974 Immune	Other Immune Function	Microarray
SLPI	Hs.251754 Immune	Other Immune Function	Microarray
SPAP1	Hs.194976 Immune	Other Immune Function	
SPN	Hs.80738 Immune	Other Immune Function	Both Databases
SYK	Hs.74101 Immune	Other Immune Function	Both Databases
TA-NFKBH	Hs.60088 Immune	Other Immune Function	EST
TBK1	Hs.21712 Immune	Other Immune Function	EST
TCIRG1	Hs.46465 Immune	Other Immune Function	Both Databases
THPO	Hs.1166 Immune	Other Immune Function	Microarray
TIMP2	Hs.6441 Immune	Other Immune Function	2.
TIMP3	Hs.245188 Immune	Other Immune Function	Microarray
TIMP4	Hs.190787 Immune	Other Immune Function	
TLR1	Hs.2474 Immune	Other Immune Function	
TLR10	Hs.120551 Immune	Other Immune Function	Microarray
TLR2	Hs.63668 Immune	Other Immune Function	Both Databases
TLR3	Hs.29499 Immune	Other Immune Function	
TMSB4X	Hs.75968 Immune	Other Immune Function	Both Databases
TOLLIP	Hs.25413 Immune	Other Immune Function	Both Databases
TPT1	Hs.401448 Immune	Other Immune Function	EST
TRAF3	Hs.297660 Immune	Other Immune Function	EST
TRIM	Hs.138701 Immune	Other Immune Function	EST
TRIP	Hs.21254 Immune	Other Immune Function	Both Databases
TYROBP	Hs.9963 Immune	Other Immune Function	Both Databases
VDR	Hs.2062 Immune	Other Immune Function	Microarray
WAS	Hs.2157 Immune	Other Immune Function	Both Databases
WASF1	Hs.75850 Immune	Other Immune Function	Microarray
ZAP-70	Hs.234569 Immune	Other Immune Function	EST
AIF1	Hs.76364 Immune	Regulated by Cytokines	Microarray
CARP	Hs.355934 Immune	Regulated by Cytokines	EST
CISH	Hs.8257 Immune	Regulated by Cytokines	Both Databases
GBP2	Hs.171862 Immune	Regulated by Cytokines	Both Databases
	Hs.380444 Immune	Regulated by Cytokines	Both Batabases
IL411		Regulated by Cytokines	Microarray
NOS2A PDCD4	Hs.193788 Immune Hs.326248 Immune	Regulated by Cytokines Regulated by Cytokines	EST
		Regulated by Cytokines	Microarray
PTX3	Hs.2050 Immune Hs.109225 Immune	Regulated by Cytokines	whorouray
VCAM1		Regulates Cytokine Activity	
ATRN	Hs.194019 Immune	Regulates Cytokine Activity	EST
BRE	Hs.80426 Immune Hs.198998 Immune	Regulates Cytokine Activity Regulates Cytokine Activity	EST
CHUK		<u> </u>	Microarray
CLEC2	Hs.114231 Immune	Regulates Cytokine Activity	IVIIGIUALTAY

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CRP	Hs.76452 Immune	Regulates Cytokine Activity	Microarray
IL18BP	Hs.325978 Immune	Regulates Cytokine Activity	EST
IL18RAP	Hs.158315 Immune	Regulates Cytokine Activity	
IL1RAP	Hs.173880 Immune	Regulates Cytokine Activity	EST
IL1RAPL1	Hs.241385 Immune	Regulates Cytokine Activity	Microarray
IL1RAPL2	Hs.272354 Immune	Regulates Cytokine Activity	Microarray
IL1RN	Hs.81134 Immune	Regulates Cytokine Activity	EST
LOC134728	Hs.158465 Immune	Regulates Cytokine Activity	
PACE4	Hs.170414 Immune	Regulates Cytokine Activity	
SOCS1.	Hs.50640 Immune	Regulates Cytokine Activity	Microarray
SOCS2	Hs.405946 Immune	Regulates Cytokine Activity	EST
SOCS3	Hs.345728 Immune	Regulates Cytokine Activity	Both Databases
TLR4	Hs.159239 Immune	Regulates Cytokine Activity	Both Databases
TLR5	Hs.114408 Immune	Regulates Cytokine Activity	
TLR6	Hs.227105 Immune	Regulates Cytokine Activity	
TLR7	Hs.179152 Immune	Regulates Cytokine Activity	Microarray
TLR8	Hs.272410 Immune	Regulates Cytokine Activity	Microarray
TLR9	Hs.87968 Irnmune	Regulates Cytokine Activity	Microarray
CAMLG	Hs.13572 Immune	T-cell Activation	· · · · · · · · · · · · · · · · · · ·
DPP4	Hs.44926 Immune	T-cell Activation	
DPP8	Hs.44033 Immune	T-cell Activation	
DUSP14	Hs.91448 Immune	T-cell Activation	EST
LCP2	Hs.2488 Immune	T-cell Activation	EST
SPP1	Hs.313 Immune	T-cell Activation	EST
AGER	Hs.184 Neuronal	Amyloid functioning	Microarray
APBA1	Hs.4880 Neuronal	Amyloid functioning	Microarray
APBA2	Hs.26468 Neuronal	Amyloid functioning	EST
APBA3	Hs.17528 Neuronal	Amyloid functioning	Both Databases
APLP1	Hs.74565 Neuronal	Amyloid functioning	Don't Databases
APOC2	Hs.75615 Neuronal	Amyloid functioning	
APP	Hs.177486 Neuronal	Amyloid functioning	Microarray
BACE	Hs.49349 Neuronal	Amyloid functioning	Microarray
BACE2	Hs.271411 Neuronal	Amyloid functioning	Microarray
ITM2B	Hs.239625 Neuronal	Amyloid functioning	Both Databases
NCSTN	Hs.4788 Neuronal	Amyloid functioning	EST
		_	Microarray
PSEN1 PTMA	Hs.3260 Neuronal Hs.250655 Neuronal	Amyloid functioning Amyloid functioning	EST
		Amyloid functioning Amyloid functioning	231
SAA2 SEMA4C	Hs.336462 Neuronal Hs.7188 Neuronal	Amyloid functioning Amyloid functioning	Both Databases
SHC1	Hs.81972 Neuronal	Amyloid functioning Amyloid functioning	Both Databases
	Hs.151123 Neuronal	Amyloid functioning Amyloid functioning	Microarray
SHC3 VSNL1		Amyloid functioning Amyloid functioning	Microarray
ADCYAP1	Hs.2288 Neuronal Hs.68137 Neuronal	Neurotransmitter	Microarray
CALCRL	Hs.152175 Neuronal	Neurotransmitter	Microarray
CALURE CBLN1		Neurotransmitter	Microarray
		Neurotransmitter	wiicioarray
KNG MAOB	Hs.77741 Neuronal Hs.82163 Neuronal	Neurotransmitter	Microarray
	Hs.345721 Neuronal	Neurotransmitter	Microarray
NPB NPFF	Hs.104555 Neuronal	Neurotransmitter	Microarray
	Hs.75640 Neuronal	Neurotransmitter	Microarray
NPPA	115.7 JU4U NEUTONAL		**************************************

NPPB Hs.247916 Neuronal Neurotransmitter Neurotransmitter Microarray Microarray NPY Hs.1832 Neuronal Neurotransmitter Neurotransmitter Microarray Microarray NTS Hs.90962 Neuronal Hs.343660 Neuronal PENK Neurotransmitter Neurotransmitter PENK Hs.93557 Neuronal PPYRT Hs.54426 Neuronal REFRP Neurotransmitter Neurotransmitter POOC Hs.89040 Neuronal PPYRT Hs.54426 Neuronal REFRP Neurotransmitter Neurotransmitter RFRP Hs.64426 Neuronal Neurotransmitter Neurotransmitter Microarray PYNTA Hs.54426 Neuronal Neurotransmitter Neurotransmitter Microarray RFRP Hs.64426 Neuronal Neurotransmitter Neurotransmitter Microarray ACHE Hs.154485 Neuronal ALDH541 Neurotransmitter Neurotransmitter Microarray ALDH541 Hs.575 Neuronal Neurotransmitter Metabolism Neurotransmitter Metabolism Microarray CHAT Hs.302002 Neuronal CPT Neurotransmitter Metabolism Neurotransmitter Metabolism Neurotransmitter Metabolism CROT Hs.172068 Neuronal SPATA Neurotransmitter Metabolism Neurotrans	***************************************	·×		***************************************
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CHAT Hs.302002 Neuronal Neurotransmitter Metabolism Microarray COMT Hs.240013 Neuronal Neurotransmitter Metabolism EST CPE Hs.75360 Neuronal Neurotransmitter Metabolism EST CPT1C Hs.112195 Neuronal Neurotransmitter Metabolism Microarray CPT2 Hs.27436 Neuronal Neurotransmitter Metabolism Microarray CRAT Hs.12068 Neuronal Neurotransmitter Metabolism Microarray CROT Hs.17978 Neuronal Neurotransmitter Metabolism Microarray DBH Hs.2301 Neuronal Neurotransmitter Metabolism Microarray DBH Hs.2301 Neuronal Neurotransmitter Metabolism Microarray DDC Hs.150403 Neuronal Neurotransmitter Metabolism Microarray GAD1 Hs.324784 Neuronal Neurotransmitter Metabolism Microarray HMOX1 Hs.284279 Neuronal Neurotransmitter Metabolism Both Databases LNPEP Hs.166733 Neuronal Neurotransmitter Metabolism Microarray NOS1 Hs.46752 Neuronal Neurotransmitter Metabolism	ALDH5A1	Hs.5299 Neuronal	Neurotransmitter Metabolism	-
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GABRB1 Hs.89768 Neuronal Neurotransmitter Receptor GABRB3 Hs.1440 Neuronal Neurotransmitter Receptor GABRD Hs.113882 Neuronal Neurotransmitter Receptor GABRE Hs.22785 Neuronal Neurotransmitter Receptor GABRG2 Hs.7195 Neuronal Neurotransmitter Receptor GABRG3 Hs.104133 Neuronal Neurotransmitter Receptor	GABRA5	Hs.24969 Neuronal	Neurotransmitter Receptor	
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GABRG3 Hs.104133 Neuronal Neurotransmitter Receptor	GABRE	Hs.22785 Neuronal		Microarray
GABRG3 Hs.104133 Neuronal Neurotransmitter Receptor	GABRG2	Hs.7195 Neuronal	Neurotransmitter Receptor	
·	GABRG3			
GADAF 75.70725 Neuronal Neuronansimile Neceptor Microarray	GABRP	Hs.70725 Neuronal	Neurotransmitter Receptor	Microarray
GABRQ Hs.283081 Neuronal Neurotransmitter Receptor			•	•
GABRR1 Hs.1438 Neuronal Neurotransmitter Receptor				
GABRR2 Hs.99927 Neuronal Neurotransmitter Receptor Microarray				Microarray
GALR1 Hs.272191 Neuronal Neurotransmitter Receptor				•
GLRA1 Hs.121490 Neuronal Neurotransmitter Receptor			•	

GPR10	Hs.248119 Neuronal	Neurotransmitter Receptor	Microarray
GRIA1	Hs.319467 Neuronal	Neurotransmitter Receptor	
GRIA2	Hs.89582 Neuronal	Neurotransmitter Receptor	
GRIA3	Hs.100014 Neuronal	Neurotransmitter Receptor	Microarray
GRIA4	Hs.163697 Neuronal	Neurotransmitter Receptor	
GRID2	Hs.248130 Neuronal	Neurotransmitter Receptor	Microarray
GRM1	Hs.32945 Neuronal	Neurotransmitter Receptor	Microarray
GRM2	Hs.121510 Neuronal	Neurotransmitter Receptor	
GRM3	Hs.3786 Neuronal	Neurotransmitter Receptor	
GRM4	Hs.178078 Neuronal	Neurotransmitter Receptor	
GRM5	Hs.167185 Neuronal	Neurotransmitter Receptor	Microarray
GRM6	Hs.248131 Neuronal	Neurotransmitter Receptor	Microarray
GRM7	Hs.83407 Neuronal	Neurotransmitter Receptor	
GRM8	Hs.86204 Neuronal	Neurotransmitter Receptor	
GRPR	Hs.73883 Neuronal	Neurotransmitter Receptor	Microarray
HCRTR1	Hs.150968 Neuronal	Neurotransmitter Receptor	
HCRTR2	Hs.151624 Neuronal	Neurotransmitter Receptor	Microarray
HTR1A	Hs.247940 Neuronal	Neurotransmitter Receptor	
HTR1B	Hs.123016 Neuronal	Neurotransmitter Receptor	
HTR1D	Hs.121482 Neuronal	Neurotransmitter Receptor	
HTR1E	Hs.1611 Neuronal	Neurotransmitter Receptor	
HTR1F	Hs.248136 Neuronal	Neurotransmitter Receptor	Microarray
HTR2A	Hs.298623 Neuronal	Neurotransmitter Receptor	Microarray
HTR2B	Hs.2507 Neuronal	Neurotransmitter Receptor	Microarray
HTR2C	Hs.46362 Neuronal	Neurotransmitter Receptor	Microarray
HTR3A	Hs.2142 Neuronal	Neurotransmitter Receptor	•
HTR3B	Hs.241377 Neuronal	Neurotransmitter Receptor	Microarray
HTR3C	Hs.352185 Neuronal	Neurotransmitter Receptor	
HTR4	Hs.113262 Neuronal	Neurotransmitter Receptor	Microarray
HTR5A	Hs.248137 Neuronal	Neurotransmitter Receptor	
HTR6	Hs.22180 Neuronal	Neurotransmitter Receptor	Microarray
HTR7	Hs.73739 Neuronal	Neurotransmitter Receptor	Microarray
NPGPR	Hs.99231 Neuronal	Neurotransmitter Receptor	Microarray
NPR2	Hs.78518 Neuronal	Neurotransmitter Receptor	•
NPR3	Hs.123655 Neuronal	Neurotransmitter Receptor	
NPY1R	Hs.169266 Neuronal	Neurotransmitter Receptor	
NPY2R	Hs.37125 Neuronal	Neurotransmitter Receptor	
NPY5R	Hs.158330 Neuronal	Neurotransmitter Receptor	
NTSR2	Hs.131138 Neuronal	Neurotransmitter Receptor	
OT7T022	Hs.302026 Neuronal	Neurotransmitter Receptor	Microarray
PNR	Hs.248198 Neuronal	Neurotransmitter Receptor	Microarray
SLC6A4	Hs.553 Neuronal	Neurotransmitter Receptor	•
TACR2	Hs.161305 Neuronal	Neurotransmitter Receptor	
Tar1	Hs.375030 Neuronal	Neurotransmitter Receptor	
VIPR2	Hs.2126 Neuronal	Neurotransmitter Receptor	Microarray
EFNA1	Hs.399713 Neuronal	Other Neuronal Function	
EFNA1	Hs.158306 Neuronal	Other Neuronal Function	Microarray
EFNA3	Hs.37054 Neuronal	Other Neuronal Function	Microarray
EFNA4	Hs.3796 Neuronal		Both Databases
EFNA5	Hs.37142 Neuronal		Microarray

EFNB1 Hs.144700 Neuronal Other Neuronal Function Microarray EFNB2 Hs.30942 Neuronal Other Neuronal Function Microarray EFNB3 Hs.26988 Neuronal Other Neuronal Function Microarray EPHA1 Hs.89839 Neuronal Other Neuronal Function Microarray EPHA2 Hs.171596 Neuronal Other Neuronal Function Microarray EPHA3 Hs.123642 Neuronal Other Neuronal Function Microarray EPHA4 Hs.73964 Neuronal Other Neuronal Function Microarray EPHA5 Hs.31092 Neuronal Other Neuronal Function Microarray EPHA6 Hs.37962 Neuronal Other Neuronal Function Other Neuronal Function EPHA7 Hs.283613 Neuronal Other Neuronal Function Other Neuronal Function EPHB1 Hs.225124 Neuronal Other Neuronal Function Microarray EPHB2 Hs.155227 Neuronal Other Neuronal Function Microarray PLXNB1 Hs.278311 N
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EPHB3 Hs.2913 Neuronal Other Neuronal Function EPHB4 Hs.155227 Neuronal Other Neuronal Function GFAP Hs.406397 Neuronal Other Neuronal Function PLXNB1 Hs.278311 Neuronal Other Neuronal Function PLXNC1 Hs.286229 Neuronal Other Neuronal Function SEMA3A Hs.2414 Neuronal Other Neuronal Function SEMA3B Hs.82222 Neuronal Other Neuronal Function SEMA3C Hs.171921 Neuronal Other Neuronal Function SEMA3D Hs.374773 Neuronal Other Neuronal Function SEMA3E Hs.212414 Neuronal Other Neuronal Function SEMA3F Hs.32981 Neuronal Other Neuronal Function SEMA4B Hs.9598 Neuronal Other Neuronal Function SEMA4F Hs.25887 Neuronal Other Neuronal Function SEMA4G Hs.169549 Neuronal Other Neuronal Function SEMA5A Hs.27621 Neuronal Other Neuronal Function SEMA5B Hs.61384 Neuronal Other Neuronal Function SEMA5B Hs.61384 Neuronal Other Neuronal Function SEMA6A Hs.263395 Neuronal Other Neuronal Function
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EREG Hs.115263 Other Growth Factor EST FGF1 Hs.75297 Other Growth Factor			Growth Factor	
FGF1 Hs.75297 Other Growth Factor				EST
				Microarray

FGF3	Hs.37092 Other	Growth Factor	Microarray
FIGF	Hs.11392 Other	Growth Factor	
GDF10	Hs.2171 Other	Growth Factor	Microarray
HGF	Hs.396530 Other	Growth Factor	
IGF1	Hs.85112 Other	Growth Factor	
IGF2	Hs.349109 Other	Growth Factor	Microarray
MDK	Hs.82045 Other	Growth Factor	
MST1	Hs.349110 Other	Growth Factor	Microarray
NELL2	Hs.79389 Other	Growth Factor	Both Databases
NGFB	Hs.2561 Other	Growth Factor	Microarray
NMB	Hs.83321 Other	Growth Factor	Microarray
NRG1	Hs.172816 Other	Growth Factor	Both Databases
NRTN	Hs.234775 Other	Growth Factor	
PDGFA	Hs.37040 Other	Growth Factor	
PDGFB	Hs.1976 Other	Growth Factor	Microarray
PDGFC	Hs.43080 Other	Growth Factor	EST
PTN	Hs.44 Other	Growth Factor	
TGFA	Hs.170009 Other	Growth Factor	Microarray
TGFB1	Hs.1103 Other	Growth Factor	Both Databases
TGFB2	Hs.169300 Other	Growth Factor	
TGFB3	Hs.2025 Other	Growth Factor	
EGFR	Hs.77432 Other	Growth Factor Receptor	Microarray
ERBB2	Hs.323910 Other	Growth Factor Receptor	Microarray
ERBB3	Hs.199067 Other	Growth Factor Receptor	
IGF1R	Hs.239176 Other	Growth Factor Receptor	
MET	Hs.419124 Other	Growth Factor Receptor	
NMBR	Hs.79042 Other	Growth Factor Receptor	
NRP2	Hs.17778 Other	Growth Factor Receptor	EST
NTRK1	Hs.406293 Other	Growth Factor Receptor	
NTRK2	Hs.47860 Other	Growth Factor Receptor	Microarray
NTRK3	Hs.26776 Other	Growth Factor Receptor	Microarray
PDGFRA	Hs.74615 Other	Growth Factor Receptor	9
PDGFRB	Hs.76144 Other	Growth Factor Receptor	EST
PDGFRL	Hs.170040 Other	Growth Factor Receptor	Microarray
CRYAB	Hs,391270 Other	Heat shock	
HARC	Hs.128646 Other	Heat shock	Microarray
HSP105B	Hs.36927 Other	Heat shock	Both Databases
HSPA1A	Hs.75452 Other	Heat shock	EST
HSPA1B	Hs.274402 Other	Heat shock	Both Databases
HSPA1L	Hs.80288 Other	Heat shock	Microarray
HSPA2	Hs.432648 Other	Heat shock	
HSPA4	Hs.90093 Other	Heat shock	Microarray
HSPA5	Hs.75410 Other	Heat shock	EST
HSPA6	Hs.3268 Other	Heat shock	Both Databases
HSPA8	Hs.180414 Other	Heat shock	Both Databases
HSPA9B	Hs.3069 Other	Heat shock	EST
HSPB2	Hs.78846 Other	Heat shock	
HSPB3	Hs.41707 Other	Heat shock	
HSPB7	Hs.56874 Other	Heat shock	
HSPCA	Hs.356531 Other	Heat shock	EST

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HSPCB	Hs.74335 Other	Heat shock	Both Databases
HSPD1	Hs.79037 Other	Heat shock	
HSPE1	Hs.1197 Other	Heat shock	EST
TRPV2	Hs.279746 Other	Heat shock	EST
ACCN3	Hs.98547 Other	Homeostasis & Small Molecule transport	Both Databases
CACNA1B	Hs.69949 Other	Homeostasis & Small Molecule transport	
CACNA1D	Hs.23838 Other	Homeostasis & Small Molecule transport	Microarray
CACNB1	Hs.635 Other	Homeostasis & Small Molecule transport	
CACNB2	Hs.30941 Other	Homeostasis & Small Molecule transport	Microarray
CACNB3	Hs.250712 Other	Homeostasis & Small Molecule transport	Microarray
CACNB4	Hs.21903 Other	Homeostasis & Small Molecule transport	
CACNG2	Hs.268545 Other	Homeostasis & Small Molecule transport	Microarray
CFTR	Hs.663 Other	Homeostasis & Small Molecule transport	
GCK	Hs.1270 Other	Homeostasis & Small Molecule transport	Microarray
GCKR	Hs.89771 Other	Homeostasis & Small Molecule transport	
RGN	Hs.77854 Other	Homeostasis & Small Molecule transport	
SCN1A	Hs.22654 Other	Homeostasis & Small Molecule transport	,
SCN1B	Hs.170238 Other	Homeostasis & Small Molecule transport	1
SCN2A2	Hs.54499 Other	Homeostasis & Small Molecule transport	Microarray
SCN2B	Hs.129783 Other	Homeostasis & Small Molecule transport	Microarray
SCN3A	Hs.300717 Other	Homeostasis & Small Molecule transport	-
SCN4A	Hs.46038 Other	Homeostasis & Small Molecule transport	L,
SCN5A	Hs.169331 Other	Homeostasis & Small Molecule transport	
SCN7A	Hs.406684 Other	Homeostasis & Small Molecule transport	
SCN9A	Hs.2319 Other	Homeostasis & Small Molecule transport	
SLC11A1	Hs.182611 Other	Homeostasis & Small Molecule transport	
SLC11A2	Hs.57435 Other	Homeostasis & Small Molecule transport	
SLC15A2	Hs.182575 Other	Homeostasis & Small Molecule transport	
SLC22A5	Hs.15813 Other	Homeostasis & Small Molecule transport	
SLC25A3	Hs.78713 Other	Homeostasis & Small Molecule transport	
SLC25A4	Hs.2043 Other	Homeostasis & Small Molecule transport	
SLC25A5	Hs.79172 Other	Homeostasis & Small Molecule transport	-
SLC29A1	Hs.25450 Other	Homeostasis & Small Molecule transport	
SLC2A11	Hs.9475 Other	Homeostasis & Small Molecule transport	
SLC2A4	Hs.95958 Other	Homeostasis & Small Molecule transport	
TRPM2	Other	Homeostasis & Small Molecule transport	•
TRPV1	Hs.283010 Other	Homeostasis & Small Molecule transport	
UGTREL1	Hs.154073 Other	Homeostasis & Small Molecule transport	
VDAC2	Hs.78902 Other	Homeostasis & Small Molecule transport	•
VDAC3	Hs.7381 Other	Homeostasis & Small Molecule transport	
VIAAT	Hs.179080 Other	Homeostasis & Small Molecule transport	
ALOXE3	Hs.232770 Other	Other	Microarray
CSTA	Hs.412999 Other	Other	moroarray
F3	Hs.62192 Other	Other	Microarray
FADS1	Hs.132898 Other	Other	Both Databases
FURIN	Hs.59242 Other	Other	Both Databases
LOC56920	Hs.59729 Other	Other	Microarray
PLTP	Hs.283007 Other	Other	Both Databases
POLE4	Hs.19980 Other	Other	Microarray
PPARGC1	Hs.198468 Other	Other	wholoarray
FFARGUI	1 15. 130400 Utilet		CONTRACTOR OF THE PROPERTY OF

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PSAP	Hs.406455 Other	Other	EST
RPS10	Hs.356491 Other	Other	
RPS5	Hs.356019 Other	Other	EST
SSBP1	Hs.923 Other	Other	Both Databases
TIMM23	Hs.11866 Other	Other	EST
TRO	Hs.259802 Other	Other	Microarray
TXNIP	Hs.179526 Other	Other	Both Databases
UBB	Hs.356190 Other	Other	EST
UBC	Hs.183704 Other	Other	EST
CADPS	Hs.151301 Other	Other Neuroendocrine Function	Microarray
CALCA	Hs.37058 Other	Other Neuroendocrine Function	Microarray
CALCB	Hs.274534 Other	Other Neuroendocrine Function	
DLG3	Hs.11101 Other	Other Neuroendocrine Function	Both Databases
DLK1	Hs.169228 Other	Other Neuroendocrine Function	Microarray
EPHX2	Hs.113 Other	Other Neuroendocrine Function	•
GMFB	Hs.151413 Other	Other Neuroendocrine Function	Microarray
GMFG	Hs.5210 Other	Other Neuroendocrine Function	Both Databases
HIP1	Hs.97206 Other	Other Neuroendocrine Function	
IAPP	Hs.142255 Other	Other Neuroendocrine Function	
INSM1	Hs.89584 Other	Other Neuroendocrine Function	
PRX	Hs.205457 Other	Other Neuroendocrine Function	4:
PTPRN	Hs.89655 Other	Other Neuroendocrine Function	Microarray
RAMP1	Hs.32989 Other	Other Neuroendocrine Function	Microarray
RAMP2	Hs.155106 Other	Other Neuroendocrine Function	Microarray
RAMP3	Hs.25691 Other	Other Neuroendocrine Function	Microarray
RCP9	Hs.300684 Other	Other Neuroendocrine Function	Microarray
RTN1	Hs.99947 Other	Other Neuroendocrine Function	Whorbarray
RTN2	Hs.3803 Other	Other Neuroendocrine Function	Both Databases
RTN3	Hs.252831 Other	Other Neuroendocrine Function	Both Databases
RTN4	Hs.65450 Other	Other Neuroendocrine Function	EST
SCAMP2	Hs.238030 Other	Other Neuroendocrine Function	Both Databases
SCG2	Hs.75426 Other	Other Neuroendocrine Function	Don't Balabacco
SCGB1A1	Hs.2240 Other	Other Neuroendocrine Function	
SCGN	Hs.116428 Other	Other Neuroendocrine Function	Microarray
SCP2	Hs.75760 Other	Other Neuroendocrine Function	EST
SGNE1	Hs.2265 Other	Other Neuroendocrine Function	Both Databases
SNAP23	Hs.184376 Other	Other Neuroendocrine Function	Both Databases
SNAP29	Hs.194714 Other	Other Neuroendocrine Function	Doin Databases
SR-BP1	Hs.24447 Other	Other Neuroendocrine Function	Both Databases
SYP	Hs.75667 Other	Other Neuroendocrine Function	Doin Databases
TFRC	Hs.77356 Other	Other Neuroendocrine Function	EST
TLOC1	Hs.8146 Other	Other Neuroendocrine Function	Both Databases
UCHL1	Hs.76118 Other	Other Neuroendocrine Function	Microarray
A2M	Hs.74561 Other	Protease Inhibitor	EST
CST3	Hs.304682 Other	Protease Inhibitor	EST
CST3	Hs.143212 Other	Protease Inhibitor	Both Databases
		Protease Inhibitor	Doin Databases
LOC139216	Hs.447335 Other		Microarroy
SERPINA6	Hs.1305 Other	Protesse Inhibitor	Microarray
SERPINE1	Hs.82085 Other	Protease Inhibitor	Microarray
TFPI	Hs.170279 Other	Protease Inhibitor	

TFPI2	Hs.295944 Other	Protease Inhibitor	
TIMP1	Hs.433425 Other	Protease Inhibitor	EST
ALOX15B	Hs.111256 Other	Regulation of Cell Growth	
ATM	Hs.194382 Other	Regulation of Cell Growth	Microarray
CDC37	Hs.160958 Other	Regulation of Cell Growth	Both Databases
CDKN1A	Hs.179665 Other	Regulation of Cell Growth	Both Databases
DUSP1	Hs.171695 Other	Regulation of Cell Growth	Both Databases
DUSP10	Hs.177534 Other	Regulation of Cell Growth	Both Databases
DUSP11	Hs.14611 Other	Regulation of Cell Growth	EST
DUSP12	Hs.44229 Other	Regulation of Cell Growth	
DUSP13	Hs.178170 Other	Regulation of Cell Growth	Microarray
DUSP15	Hs.375624 Other	Regulation of Cell Growth	•
DUSP18	Hs.128782 Other	Regulation of Cell Growth	EST
DUSP19	Hs.132237 Other	Regulation of Cell Growth	
DUSP2	Hs.1183 Other	Regulation of Cell Growth	Both Databases
DUSP21	Hs.15572 Other	Regulation of Cell Growth	Microarray
DUSP22	Hs.29106 Other	Regulation of Cell Growth	Both Databases
DUSP3	Hs.181046 Other	Regulation of Cell Growth	Both Batabases
DUSP4	Hs.2359 Other	Regulation of Cell Growth	Both Databases
	Hs.2128 Other	•	EST
DUSP5		Regulation of Cell Growth	
DUSP6	Hs.180383 Other	Regulation of Cell Growth	EST
DUSP7	Hs.296938 Other	Regulation of Cell Growth	· •
DUSP9	Hs.144879 Other	Regulation of Cell Growth	
EPS15	Hs.79095 Other	Regulation of Cell Growth	EST
EPS15R	Hs.147176 Other	Regulation of Cell Growth	EST
GFRA2	Hs.19317 Other	Regulation of Cell Growth	
GRB7	Hs.86859 Other	Regulation of Cell Growth	Microarray
HGFAC	Hs.104 Other	Regulation of Cell Growth	,
HGS	Hs.416959 Other	Regulation of Cell Growth	•
IGFBP2	Hs.433326 Other	Regulation of Cell Growth	
IGFBP3	Hs.77326 Other	Regulation of Cell Growth	Microarray
IGFBP4	Hs.1516 Other	Regulation of Cell Growth	
IGFBP5	Hs.416739 Other	Regulation of Cell Growth	
IGFBP6	Hs.274313 Other	Regulation of Cell Growth	Microarray
KIT	Hs.81665 Other	Regulation of Cell Growth	
MT1H	Hs.2667 Other	Regulation of Cell Growth	
MT2A	Hs.118786 Other	Regulation of Cell Growth	
MT3	Hs.73133 Other	Regulation of Cell Growth	Microarray
MYC	Hs.79070 Other	Regulation of Cell Growth	Both Databases
NGFRAP1	Hs.381039 Other	Regulation of Cell Growth	
NRG2	Hs.113264 Other	Regulation of Cell Growth	Microarray
NTF3	Hs.99171 Other	Regulation of Cell Growth	·
NTF5	Hs.266902 Other	Regulation of Cell Growth	
PAPPA	Hs.75874 Other	Regulation of Cell Growth	
PLG	Hs.75576 Other	Regulation of Cell Growth	
PPM1A	Hs.57764 Other	Regulation of Cell Growth	EST
PPM1D	Hs.100980 Other	Regulation of Cell Growth	
PRSS11	Hs.75111 Other	Regulation of Cell Growth	Both Databases
PSPN	Hs.248159 Other	Regulation of Cell Growth	Microarray
PTCH	Hs.159526 Other	Regulation of Cell Growth	Microarray

PTCH2	Hs.249164 Other	Regulation of Cell Growth	
PTPN2	Hs.82829 Other	Regulation of Cell Growth	
PTPN3	Hs.153932 Other	Regulation of Cell Growth	Microarray
SNT-1	Hs.251394 Other	Regulation of Cell Growth	Microarray
SNT-2	Hs.194208 Other	Regulation of Cell Growth	Microarray
SPINT1	Hs.233950 Other	Regulation of Cell Growth	Both Databases
SPINT2	Hs.31439 Other	Regulation of Cell Growth	Both Databases
SRC	Hs.198298 Other	Regulation of Cell Growth	
TEK	Hs.89640 Other	Regulation of Cell Growth	Microarray
VGF	Hs.171014 Other	Regulation of Cell Growth	Microarray
WISP2	Hs.194679 Other	Regulation of Cell Growth	Microarray
WISP3	Hs.194678 Other	Regulation of Cell Growth	-
WNT1	Hs.248164 Other	Regulation of Cell Growth	
WNT10B	Hs.91985 Other	Regulation of Cell Growth	Microarray
WNT2	Hs.89791 Other	Regulation of Cell Growth	•
AIP	Hs.75305 Other	Signal Transduction	EST
AKAP9	Hs.58103 Other	Signal Transduction	Both Databases
ARRB1	Hs.112278 Other	Signal Transduction	Both Databases
BMX	Hs.27372 Other	Signal Transduction	Microarray
DUSP16	Hs.20281 Other	Signal Transduction	Both Databases
DUSP8	Hs.41688 Other	Signal Transduction	Microarray
FLT3	Hs.385 Other	Signal Transduction	····o. ca ay
FLT3LG	Hs.428 Other	Signal Transduction	Both Databases
FYB	Hs.58435 Other	Signal Transduction	Doill Balandoos
GAB2	Hs.30687 Other	Signal Transduction	Microarray
GADD45B	Hs.110571 Other	Signal Transduction	Both Databases
GFRA3	Hs.58042 Other	Signal Transduction	Doi: Databaooo
GFRA4	Hs.302025 Other	Signal Transduction	Microarray
GRAP2	Hs.193076 Other	Signal Transduction	Both Databases
IL6ST	Hs.82065 Other	Signal Transduction	Microarray
IRAK1	Hs.182018 Other	Signal Transduction	Both Databases
IRAK2	Hs.249175 Other	Signal Transduction	Microarray
IRAK3	Hs.268552 Other	Signal Transduction	Wildroditay
IRAK4	Hs.142295 Other	Signal Transduction	EST
ITK	Hs.211576 Other	Signal Transduction	Both Databases
JAK1	Hs.50651 Other	Signal Transduction	Both Batabases
JAK2	Hs.115541 Other	Signal Transduction	
JAK3	Hs.99877 Other	Signal Transduction	Both Databases
LCK	Hs.1765 Other	Signal Transduction	EST
LOC55971	Hs.23449 Other	Signal Transduction	Microarray
MAP2K1	Hs.3446 Other	Signal Transduction	EST
MAP2K3	Hs.180533 Other	Signal Transduction	Both Databases
MAP2K4	Hs.75217 Other	Signal Transduction	Microarray
MAP2K6	Hs.118825 Other	Signal Transduction Signal Transduction	Microarray
MAP2K7	Hs.110299 Other	Signal Transduction	wiioroarray
MAP3K10	Hs.30223 Other	Signal Transduction Signal Transduction	Microarray *
MAP3K10	Hs.89449 Other	Signal Transduction Signal Transduction	Both Databases
MAP3K11		Signal Transduction Signal Transduction	EST
	Hs.211601 Other	_	LOI
MAP3K13	Hs.377067 Other	Signal Transduction	
MAP3K2	Hs.28827 Other	Signal Transduction	

марзкз	Hs.29282 Other	Signal Transduction	Both Databases
MAP3K4	Hs.32353 Other	Signal Transduction	Microarray
MAP3K7	Hs.7510 Other	Signal Transduction	Microarray
MAP3K8	Hs.248 Other	Signal Transduction	EST
MAP4K1	Hs.95424 Other	Signal Transduction	EST
MAP4K3	Hs.399752 Other	Signal Transduction	
MAPK1	Hs.324473 Other	Signal Transduction	EST
MAPK10	Hs.151051 Other	Signal Transduction	Microarray
MAPK13	Hs.178695 Other	Signal Transduction	Both Databases
MAPK14	Hs.79107 Other	Signal Transduction	Both Databases
MAPK8	Hs.267445 Other	Signal Transduction	Microarray
MAPK8IP1	Hs.234249 Other	Signal Transduction	Microarray
MAPK8IP2	Hs.356523 Other	Signal Transduction	
MAPK8IP3	Hs.88500 Other	Signal Transduction	EST
MAPK9	Hs.246857 Other	Signal Transduction	201
MAPKAPK2	Hs.75074 Other	Signal Transduction	Both Databases
MATK	Hs.274 Other	Signal Transduction	EST
	Hs.99960 Other	_	201
MS4A3		Signal Transduction	EST
MS4A4A	Hs.325960 Other	Signal Transduction	E31
MS4A5	Hs.178066 Other	Signal Transduction	Dath Databases
MS4A6A	Hs.17914 Other	Signal Transduction	Both Databases
MS4A7	Hs.11090 Other	Signal Transduction	Both Databases
pknbeta	Hs.44101 Other	Signal Transduction	Microarray
PLA2G1B	Hs.992 Other	Signal Transduction	Microarray
PRKCA	Hs.169449 Other	Signal Transduction	EST
PRKCB1	Hs.77202 Other	Signal Transduction	EST
PRKCD	Hs.155342 Other	Signal Transduction	Both Databases
PRKCE	Hs.211592 Other	Signal Transduction	
PTPN6	Hs.63489 Other	Signal Transduction	Both Databases
PTPNS1	Hs.156114 Other	Signal Transduction	Both Databases
RAF1	Hs.349650 Other	Signal Transduction	EST
S100A12	Hs.19413 Other	Signal Transduction	
SCAP1	Hs.19126 Other	Signal Transduction	EST
SCAP2	Hs.52644 Other	Signal Transduction	EST
SGKL	Hs.380877 Other	Signal Transduction	
SITPEC	Hs.22199 Other	Signal Transduction	Both Databases
TEC	Hs.89656 Other	Signal Transduction	
TIRAP	Hs.17681 Other	Signal Transduction	EST
TRAF6	Hs.90957 Other	Signal Transduction	Both Databases
TYK2	Hs.75516 Other	Signal Transduction	EST
YWHAB	Hs.182238 Other	Signal Transduction	Both Databases
Cyt19	Hs.349396 Other	Stress Response	.Both Databases
GADD45A	Hs.80409 Other	Stress Response	EST
GADD45G	Hs.9701 Other	Stress Response	Microarray
GPX1	Hs.76686 Other	Stress Response	Both Databases
GSR	Hs.193974 Other	Stress Response	EST
GSTM3	Hs.2006 Other	Stress Response	EST
NR1	Hs.154899 Other	Stress Response	EST
SOD1	Hs.75428 Other	Stress Response	Both Databases
	Hs.372783 Other	Stress Response	EST
SOD2	118.312103 UHE	Oricoo izeohorioe	

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STIP1	Hs.355930 Other	Stress Response	EST
AHR	Hs.170087 Other	Transcription Factor	Microarray
ASCL1	Hs.1619 Other	Transcription Factor	Microarray
ATF2	Hs.198166 Other	Transcription Factor	
ATF3	Hs.460 Other	Transcription Factor	Both Databases
BATF	Hs.41691 Other	Transcription Factor	Both Databases
CDX1	Hs.1545 Other	Transcription Factor	
CEBPA	Hs.76171 Other	Transcription Factor	Microarray
CEBPB	Hs.99029 Other	Transcription Factor	Microarray
CEBPG	Hs.2227 Other	Transcription Factor	Microarray
CLOCK	Hs.150602 Other	Transcription Factor	EST
CNOT2	Hs.239720 Other	Transcription Factor	Both Databases
DAT1	Hs.301914 Other	Transcription Factor	
DBP	Hs.414480 Other	Transcription Factor	
DSIPI	Hs.75450 Other	Transcription Factor	EST
EGR1	Hs.326035 Other	Transcription Factor	EST
ELK1	Hs.181128 Other	Transcription Factor	Both Databases
EN1	Hs.271977 Other	Transcription Factor	Doin Balabacco
EN2	Hs.134989 Other	Transcription Factor	
ENO1	Hs.254105 Other	Transcription Factor	Both Databases
ETS1	Hs.18063 Other	Transcription Factor	EST
	Hs.25647 Other	•	Both Databases
FOS		Transcription Factor	DOIN Dalabases
FOXA1	Hs.70604 Other	Transcription Factor	Microcano
FOXA2	Hs.155651 Other	Transcription Factor	Microarray
FOXA3	Hs.36137 Other	Transcription Factor	Microarray
FOXP3	Hs.247700 Other	Transcription Factor	Microarray
GATA3	Hs.169946 Other	Transcription Factor	EST
GIOT-1	Hs.157203 Other	Transcription Factor	
GIOT-2	Hs.251371 Other	Transcription Factor	Microarray
GIOT-3	Hs.102397 Other	Transcription Factor	
GMEB2	Hs.28906 Other	Transcription Factor	Microarray
GRLF1	Hs.102548 Other	Transcription Factor	
HMGB1	Hs.434102 Other	Transcription Factor	
HOXA1	Hs.67397 Other	Transcription Factor	Microarray
HOXB1	Hs.99992 Other	Transcription Factor	Microarray
HSF1	Hs.380935 Other	Transcription Factor	EST
ICSBP1	Hs.14453 Other	Transcription Factor	Both Databases
ILF1	Hs.296281 Other	Transcription Factor	Both Databases
ILF2	Hs.75117 Other	Transcription Factor	EST
ILF3	Hs.256583 Other	Transcription Factor	Both Databases
IRF1	Hs.80645 Other	Transcription Factor	Both Databases
IRF2	Hs.83795 Other	Transcription Factor	Both Databases
IRF3	Hs.75254 Other	Transcription Factor	Both Databases
IRF5	Hs.334450 Other	Transcription Factor	EST
IRF6	Hs.11801 Other	Transcription Factor	
IRF7	Hs.166120 Other	Transcription Factor	Both Databases
ISGF3G	Hs.1706 Other	Transcription Factor	Both Databases
JUN	Hs.78465 Other	Transcription Factor	EST
JUNB	Hs.400124 Other	Transcription Factor	EST
LOC170067	Hs.447895 Other	Transcription Factor	
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MAFF	Hs.51305 Other	Transcription Factor	Microarray
MAZ	Hs.7647 Other	Transcription Factor	EST
MDM2	Hs.170027 Other	Transcription Factor	
MEF2C	Hs.78995 Other	Transcription Factor	
MIZIP	Hs.128096 Other	Transcription Factor	
NFATC3	Hs.172674 Other	Transcription Factor	EST
NFKB1	Hs.83428 Other	Transcription Factor	Microarray
NFKB2	Hs.73090 Other	Transcription Factor	EST
NFKBIA	Hs.81328 Other	Transcription Factor	Both Databases
NFKBIB	Hs.9731 Other	Transcription Factor	Both Databases
NFKBIE	Hs.182885 Other	Transcription Factor	EST
NFKBIL1	Hs.2764 Other	Transcription Factor	Both Databases
NFRKB	Hs.374357 Other	Transcription Factor	
NFX1	Hs.3187 Other	Transcription Factor	Both Databases
NMI	Hs.54483 Other	Transcription Factor	
NR1I2	Hs.118138 Other	Transcription Factor	Microarray
NRF	Hs.119018 Other	Transcription Factor	
P38IP	Hs.376447 Other	Transcription Factor	EST
PIAS1	Hs.75251 Other	Transcription Factor	Both Databases
POU1F1	Hs.89394 Other	Transcription Factor	
PRDM1	Hs.158303 Other	Transcription Factor	Microarray
RFX2	Hs.100007 Other	Transcription Factor	
SLC2A4RG	Hs.254837 Other	Transcription Factor	·
SMARCA2	Hs.198296 Other	Transcription Factor	Microarray
SMARCF1	Hs.123090 Other	Transcription Factor	Both Databases
STAT1	Hs.21486 Other	Transcription Factor	Both Databases
STAT2	Hs.72988 Other	Transcription Factor	Microarray
STAT3	Hs.321677 Other	Transcription Factor	EST
STAT4	Hs.80642 Other	Transcription Factor	EST
	Hs.167503 Other	Transcription Factor	Both Databases
STAT5A			Doin Databases
STAT5B	Hs.244613 Other	Transcription Factor	EST
STAT6	Hs.181015 Other	Transcription Factor	Both Databases
TAF9	Hs.60679 Other	Transcription Factor	BOIII Dalabases
TBX19	Hs.50403 Other	Transcription Factor	
TBX21	Hs.272409 Other	Transcription Factor	
TCF1	Hs.73888 Other	Transcription Factor	· FOT
TCF4	Hs.326198 Other	Transcription Factor	EST
TCF7	Hs.169294 Other	Transcription Factor	Microarray
TCF8	Hs.232068 Other	Transcription Factor	D # D ()
TFE3	Hs.274184 Other	Transcription Factor	Both Databases
TRIAD3	Hs.86228 Other	Transcription Factor	Microarray
TRIM34	Hs.125300 Other	Transcription Factor	Microarray
UBP1	Hs.28423 Other	Transcription Factor	Microarray
ZFP36	Hs.343586 Other	Transcription Factor	Microarray
ZFP36L1	Hs.85155 Other	Transcription Factor	Both Databases
ZIC2	Hs.132863 Other	Transcription Factor	Microarray
ZNF14	Hs.197219 Other	Transcription Factor	Microarray
ZNF147	Hs.1579 Other	Transcription Factor	EST
ZNF161	Hs.223754 Other	Transcription Factor	
ZNF259	Hs.7165 Other	Transcription Factor	EST

ZNF398	Hs.169452 Other	Transcription Factor	
EBI2	Hs.784 Other	Unknown Function	Both Databases
NFKBIL2	Hs.356764 Other	Unknown Function	EST
PTPN18	Hs.278597 Other	Unknown Function	Both Databases
WSB1	Hs.187991 Other	Unknown Function	Microarray

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 Atherosclerosis, 148(2), 209-14.

V. CLAIMS

What is claimed is:

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1. A microarray comprising probes for genes involved in pscyhoneuroendocrinimmune (PNI) activity.

- 2. The microarray of claim 1, wherein the genes are selected from the group of genes consisting of SEQ ID NO: 1-1741 and 3086-3314.
- 3. The microarray of claim 2, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1-1741 and 3086-3314, and wherein the number of genes selected is 100.
- 4. The microarray of claim 2, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1-1741 and 3086-3314, and wherein the number of genes selected is 500.
- 5. The microarray of claim 2, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1-1741 and 3086-3314, and wherein the number of genes selected is 1000.
- 6. The microarray of claim 2, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1-1741 and 3086-3314, and wherein the number of genes selected is 1500.
- 7. The microarray of claim 1, wherein the genes are selected from the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514.
- 8. The microarray of claim 7, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514, and wherein the number of genes selected is 100.
- 9. The microarray of claim 7, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514, and wherein the number of genes selected is 200.
- 10. The microarray of claim 7, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514, and wherein the number of genes selected is 500.
- 11. The microarray of claim 7, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514, and wherein the number of genes selected is 1000.

12. The microarray of claim 7, wherein the genes are selected from the the group of genes consisting of SEQ ID NO: 1742-3085 and 3315-3514, and wherein the number of genes selected is 1500.

13. A method for diagnosing a condition associated with PNI activity comprising obtaining a tissue sample from a subject, isolating RNA from the sample, placing the RNA on the microarray of any of claims 1, and analyzing the gene expression on the array.

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- 14. The method of claim 13, wherein the condition is selected from the group of PNI associated conditions consisting of CFS, type-2 diabetes, allergic conditions including atopic dermatitis, rheumatic diseases such as rheumatoid arthritis and systemic lupus erythematosus, Sjogren's syndrome, coronary heart disease, inflammatory bowel disease, acute depression, fatigue diseases resulting from defined causes, such as cancer treatment, post traumatic stress disease, susceptibility to alcoholism, Alzheimer's Disease, and cognitive impairment resulting from multiple sclerosis.
- 15. The method of claim 13, wherein the condition is an inflammatory condition.
- 16. The method of claim 15, wherein the inflammatory condition is selected from the group of inflammatory conditions consisting of asthma, alopecia areata, systemic lupus erythematosus, rheumatoid arthritis, reactive arthritis, spondylarthritis, systemic vasculitis, insulin dependent diabetes mellitus, multiple sclerosis, experimental allergic encephalomyelitis, Sjögren's syndrome, graft versus host disease, inflammatory bowel disease including Crohn's disease, ulcerative colitis, ischemia reperfusion injury, myocardial infarction, Alzheimer's disease, transplant rejection (allogeneic and xenogeneic), thermal trauma, any immune complex-induced inflammation, glomerulonephritis, myasthenia gravis, cerebral lupus, Guillain-Barre syndrome, vasculitis, systemic sclerosis, anaphlaxis, catheter reactions, atheroma, infertility, thyroiditis, ARDS, post-bypass syndrome, hemodialysis, juvenile rheumatoid, Behcets syndrome, hemolytic anemia, pemphigus, bullous pemphigoid, stroke, atherosclerosis, scleroderma, psoriasis, sarcoidosis, transverse myelitis, acute disseminated encephalomyelitis, post-infectious encephalomyelitis, subacute sclerosing panencephalitis, and chronic inflammatory demyelinating polyradiculopathy.
 - 17. The method of claim 13, wherein the condition is a cancer.

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18. The method of claim 17, wherein the cancer is selected from the group of cancers consisting of lymphoma, B cell lymphoma, T cell lymphoma, mycosis fungoides, Hodgkin's Disease, myeloid leukemia, bladder cancer, brain cancer, nervous system cancer, head and neck cancer, squamous cell carcinoma of head and neck, kidney cancer, lung cancers such as small cell lung cancer and non-small cell lung cancer, neuroblastoma/glioblastoma, ovarian cancer, pancreatic cancer, prostate cancer, skin cancer, liver cancer, melanoma, squamous cell carcinomas of the mouth, throat, larynx, and lung, colon cancer, cervical cancer, cervical carcinoma, breast cancer, and epithelial cancer, renal cancer, genitourinary cancer, pulmonary cancer, esophageal carcinoma, head and neck carcinoma, large bowel cancer, hematopoietic cancers; testicular cancer; colon and rectal cancers, prostatic cancer, or pancreatic cancer.

19. The method of claim 13, wherein the condition is an infectious disease.

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 Z_{i}^{\prime}

 $\vec{e}_1 \neq$

- 20. The method of claim 19, wherein the infectious disease is a bacterial infection selected from the group of bacteria consisting of M. tuberculosis, M. bovis, M. bovis strain BCG, BCG substrains, M. avium, M. intracellulare, M. africanum, M. kansasii, M. marinum, M. ulcerans, M. avium subspecies paratuberculosis, Nocardia asteroides, other Nocardia species, Legionella pneumophila, other Legionella species, Salmonella typhi, other Salmonella species, Shigella species, Yersinia pestis, Pasteurella haemolytica, Pasteurella multocida, other Pasteurella species, Actinobacillus pleuropneumoniae, Listeria monocytogenes, Listeria ivanovii, Brucella abortus, other Brucella species, Cowdria ruminantium, Chlamydia pneumoniae, Chlamydia trachomatis, Chlamydia psittaci, Coxiella burnetti, other Rickettsial species, Ehrlichia species, Staphylococcus aureus, Staphylococcus epidermidis, Streptococcus pyogenes, Streptococcus agalactiae, Bacillus anthracis, Escherichia coli, Vibrio cholerae, Campylobacter species, Neiserria meningitidis, Neiserria gonorrhea. Pseudomonas aeruginosa, other Pseudomonas species, Haemophilus influenzae, Haemophilus ducreyi, other Hemophilus species, Clostridium tetani, other Clostridium species, Yersinia enterolitica, and other Yersinia species.
- 21. The method of claim 19, wherein the infectious disease is a viral infection selected from the group of viruses consisting of Herpes simplex virus type-1, Herpes simplex virus type-2, Cytomegalovirus, Epstein-Barr virus, Varicella-zoster virus, Human herpesvirus 6, Human herpesvirus 7, Human herpesvirus 8, Variola virus, Vesicular stomatitis virus, Hepatitis A virus, Hepatitis B virus, Hepatitis C virus,

Hepatitis D virus, Hepatitis E virus, Rhinovirus, Coronavirus, Influenza virus A, Influenza virus B, Measles virus, Polyomavirus, Human Papilomavirus, Respiratory syncytial virus, Adenovirus, Coxsackie virus, Dengue virus, Mumps virus, Poliovirus, Rabies virus, Rous sarcoma virus, Yellow fever virus, Ebola virus, Marburg virus,

- Lassa fever virus, Eastern Equine Encephalitis virus, Japanese Encephalitis virus, St.
 Louis Encephalitis virus, Murray Valley fever virus, West Nile virus, Rift Valley fever virus, Rotavirus A, Rotavirus B, Rotavirus C, Sindbis virus, Simian Immunodeficiency cirus, Human T-cell Leukemia virus type-1, Hantavirus, Rubella virus, Simian Immunodeficiency virus, Human Immunodeficiency virus type-1, and Human Immunodeficiency virus type-2.
 - 22. The method of claim 19, wherein the infectious disease is a fungal infection selected from the group of fungi consisting of *Candida albicans*, *Cryptococcus neoformans*, *Histoplama capsulatum*, *Aspergillus fumigatus*, *Coccidiodes immitis*, *Paracoccidiodes brasiliensis*, *Blastomyces dermitidis*, *Pneomocystis carnii*, *Penicillium marneffi*, and *Alternaria alternata*.

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- 23. The method of claim 19, wherein the infectious disease is a parasitic infection selected from the group of parasites consisting of *Toxoplasma gondii*, *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium malariae*, other *Plasmodium* species., *Trypanosoma brucei*, *Trypanosoma cruzi*, *Leishmania major*, other *Leishmania* species., *Schistosoma mansoni*, other *Schistosoma* species., and *Entamoeba histolytica*.
- 24. The method of claim 13, further comprising making a diagnosis based on the pattern of gene expression on the microarray, wherein a pattern matching one associated with a condition indicates the subject has the condition.
 - 25. The method of claim 13, wherein the tissue sample is blood.
 - 26. The method of claim 13, wherein the subject is a mammal.
 - 27. The method of claim 26, wherein the mammal is a human.
 - 28. The method of claim 26, wherein the mammal is a mouse.
- 29. A method for diagnosing a condition associated with PNI activity comprising obtaining a tissue sample from a subject, isolating RNA from the sample, placing the RNA on a PNI microarray, and analyzing the gene expression on the array.
- 30. The method of claim 29, wherein the condition is selected from the group of PNI associated conditions consisting of CFS, type-2 diabetes, allergic conditions

including atopic dermatitis, rheumatic diseases such as rheumatoid arthritis and systemic lupus erythematosus, Sjogren's syndrome, coronary heart disease, inflammatory bowel disease, acute depression, fatigue diseases resulting from defined causes, such as cancer treatment, post traumatic stress disease, susceptibility to alcoholism, Alzheimer's Disease, and cognitive impairment resulting from multiple sclerosis.

31. The method of claim 29, wherein the condition is an inflammatory condition.

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- 32. The method of claim 31, wherein the inflammatory condition is selected from the group of inflammatory conditions consisting of asthma, alopecia areata, systemic lupus erythematosus, rheumatoid arthritis, reactive arthritis, spondylarthritis, systemic vasculitis, insulin dependent diabetes mellitus, multiple sclerosis, experimental allergic encephalomyelitis, Sjögren's syndrome, graft versus host disease, inflammatory bowel disease including Crohn's disease, ulcerative colitis, ischemia reperfusion injury, myocardial infarction, Alzheimer's disease, transplant rejection (allogeneic and xenogeneic), thermal trauma, any immune complex-induced inflammation, glomerulonephritis, myasthenia gravis, cerebral lupus, Guillain-Barre syndrome, vasculitis, systemic sclerosis, anaphlaxis, catheter reactions, atheroma, infertility, thyroiditis, ARDS, post-bypass syndrome, hemodialysis, juvenile rheumatoid, Behcets syndrome, hemolytic anemia, pemphigus, bullous pemphigoid, stroke, atherosclerosis, scleroderma, psoriasis, sarcoidosis, transverse myelitis, acute disseminated encephalomyelitis, post-infectious encephalomyelitis, subacute sclerosing panencephalitis, and chronic inflammatory demyelinating polyradiculopathy.
 - 33. The method of claim 29, wherein the condition is a cancer.
- 34. The method of claim 33, wherein the cancer is selected from the group of cancers consisting of lymphoma, B cell lymphoma, T cell lymphoma, mycosis fungoides, Hodgkin's Disease, myeloid leukemia, bladder cancer, brain cancer, nervous system cancer, head and neck cancer, squamous cell carcinoma of head and neck, kidney cancer, lung cancers such as small cell lung cancer and non-small cell lung cancer, neuroblastoma/glioblastoma, ovarian cancer, pancreatic cancer, prostate cancer, skin cancer, liver cancer, melanoma, squamous cell carcinomas of the mouth, throat, larynx, and lung, colon cancer, cervical cancer, cervical carcinoma, breast cancer, and epithelial cancer, renal cancer, genitourinary cancer, pulmonary cancer, esophageal

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carcinoma, head and neck carcinoma, large bowel cancer, hematopoietic cancers; testicular cancer; colon and rectal cancers, prostatic cancer, or pancreatic cancer.

- 35. The method of claim 29, wherein the condition is an infectious disease.
- 36. The method of claim 35, wherein the infectious disease is a bacterial infection selected from the group of bacteria consisting of *M. tuberculosis*, *M. bovis*, *M. bovis* strain BCG, BCG substrains, *M. avium*, *M. intracellulare*, *M. africanum*, *M. kansasii*, *M. marinum*, *M. ulcerans*, *M. avium* subspecies paratuberculosis, Nocardia asteroides, other Nocardia species, Legionella pneumophila, other Legionella species, Salmonella typhi, other Salmonella species, Shigella species, Yersinia pestis,
- Pasteurella haemolytica, Pasteurella multocida, other Pasteurella species,
 Actinobacillus pleuropneumoniae, Listeria monocytogenes, Listeria ivanovii, Brucella abortus, other Brucella species, Cowdria ruminantium, Chlamydia pneumoniae,
 Chlamydia trachomatis, Chlamydia psittaci, Coxiella burnetti, other Rickettsial species,
 Ehrlichia species, Staphylococcus aureus, Staphylococcus epidermidis, Streptococcus
 pyogenes, Streptococcus agalactiae, Bacillus anthracis, Escherichia coli, Vibrio cholerae, Campylobacter species, Neiserria meningitidis, Neiserria gonorrhea,
 Pseudomonas aeruginosa, other Pseudomonas species, Haemophilus influenzae,
 Haemophilus ducreyi, other Hemophilus species, Clostridium tetani, other Clostridium species, Yersinia enterolitica, and other Yersinia species.
- 37. The method of claim 35, wherein the infectious disease is a viral infection 20 selected from the group of viruses consisting of Herpes simplex virus type-1, Herpes simplex virus type-2, Cytomegalovirus, Epstein-Barr virus, Varicella-zoster virus, Human herpesvirus 6, Human herpesvirus 7, Human herpesvirus 8, Variola virus, Vesicular stomatitis virus, Hepatitis A virus, Hepatitis B virus, Hepatitis C virus, Hepatitis D virus, Hepatitis E virus, Rhinovirus, Coronavirus, Influenza virus A, 25 Influenza virus B, Measles virus, Polyomavirus, Human Papilomavirus, Respiratory syncytial virus, Adenovirus, Coxsackie virus, Dengue virus, Mumps virus, Poliovirus, Rabies virus, Rous sarcoma virus, Yellow fever virus, Ebola virus, Marburg virus, Lassa fever virus, Eastern Equine Encephalitis virus, Japanese Encephalitis virus, St. Louis Encephalitis virus, Murray Valley fever virus, West Nile virus, Rift Valley fever 30 virus, Rotavirus A, Rotavirus B, Rotavirus C, Sindbis virus, Simian Immunodeficiency cirus, Human T-cell Leukemia virus type-1, Hantavirus, Rubella virus, Simian

Immunodeficiency virus, Human Immunodeficiency virus type-1, and Human Immunodeficiency virus type-2.

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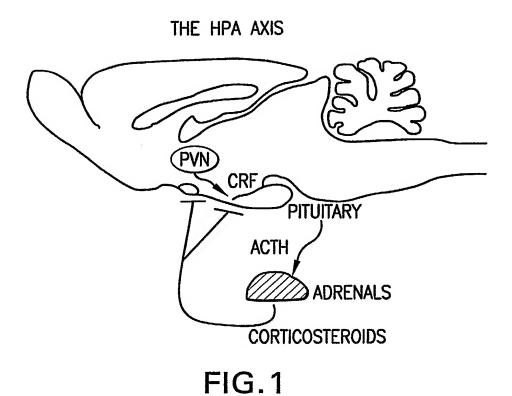
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38. The method of claim 35, wherein the infectious disease is a fungal infection selected from the group of fungi consisting of Candida albicans, Cryptococcus neoformans, Histoplama capsulatum, Aspergillus fumigatus, Coccidiodes immitis, Paracoccidiodes brasiliensis, Blastomyces dermitidis, Pneomocystis carnii, Penicillium marneffi, and Alternaria alternata.

- 39. The method of claim 35, wherein the infectious disease is a parasitic infection selected from the group of parasites consisting of *Toxoplasma gondii*, *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium malariae*, other *Plasmodium* species., *Trypanosoma brucei*, *Trypanosoma cruzi*, *Leishmania major*, other *Leishmania* species., *Schistosoma mansoni*, other *Schistosoma* species., and *Entamoeba histolytica*.
- 40. The method of claim 29, further comprising making a diagnosis based on the pattern of gene expression on the microarray, wherein a pattern matching one associated with a condition indicates the subject has the condition.
- 41. A method of identifying genes involved in a condition associated with PNI activity comprising obtaining tissue samples from subjects with the condition and a control population, isolating the RNA, analyzing the RNA using a PNI microarray, and comparing the expression of genes in the subjects with the condition to the control population, wherein gene expression present in 70% or more of the subjects, but in fewer than 20% of the controls indicates genes involved in a condition associated with PNI activity.
 - 42. The method of claim 41, wherein the tissue sample is blood.
 - 43. The method of claim 41, wherein the subject is a mammal.
 - 44. The method of claim 42, wherein the mammal is a human.
 - 45. The method of claim 42, wherein the mammal is a mouse.
- 46. A method of classifying a condition as being associated with PNI activity comprising obtaining tissue samples from subjects with the condition and a control population, isolating the RNA, analyzing the RNA using a PNI microarray, and comparing the expression of genes in the subjects with the condition to the control population, wherein conditions that result in gene expression present in 70% or more of

the subjects, but in fewer than 20% of the controls indicates a condition associated with PNI activity.



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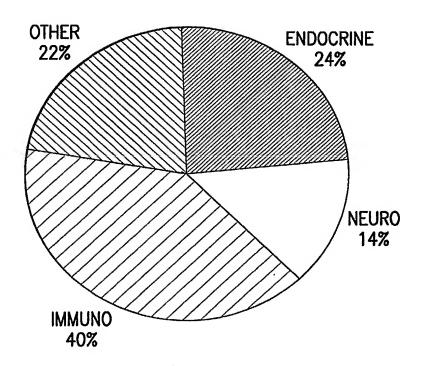
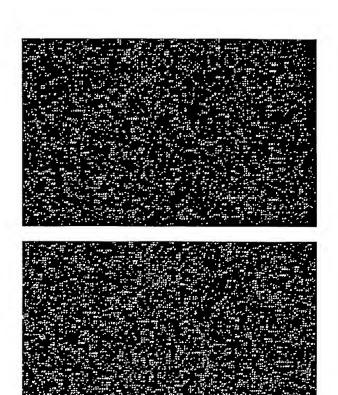


FIG.2



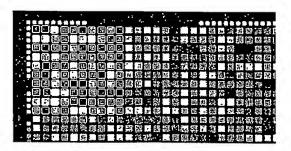
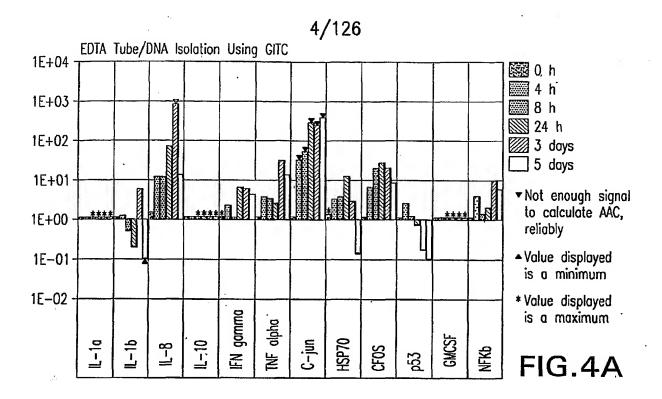
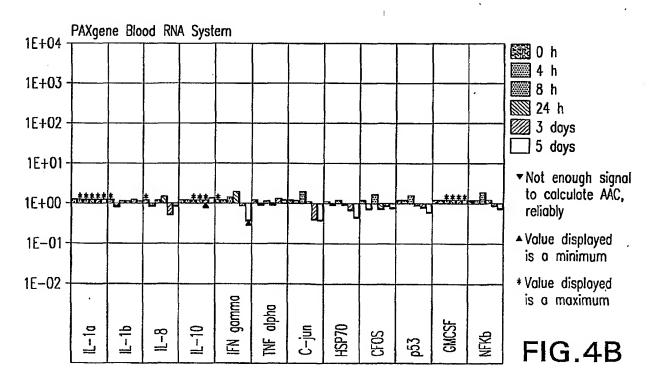


FIG.3B

FIG.3A





Blood was collected and RNA was isolated using either A standard methods (collection in EDTA tubes; no stabilization; RNA isolation using a guanidinium—based method), or B the PAXgene Blood RNA System (for RNA stabilization and isolation). The graphs show changes in expression of 12 genes after blood collection, measured using real—time RT—PCR. (Data kindly provided by Source Precision Medicine, Boulder, Colorated RIST (Fibrator Rocket).

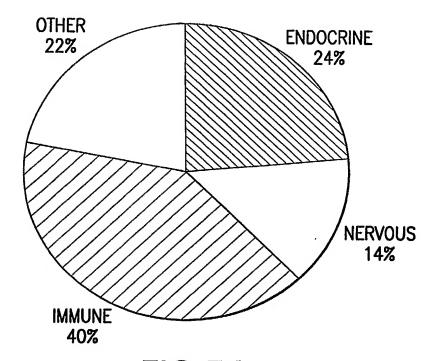
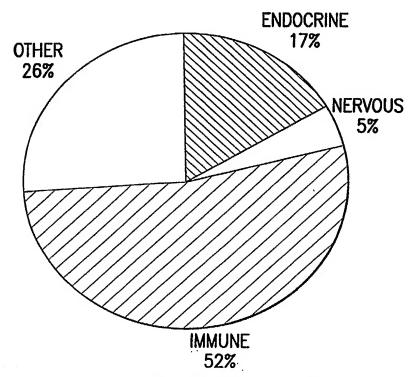


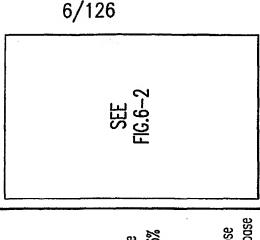
FIG.5A



SUBSTITUTE SHEET (RULE 26)

Many psychoneuroendocrinimmune genes are expressed in peripheral blood





A) All PNI Genes analyzed

B) PNI Genes with ESTs in blood

C) PNI Genes expressed in PBMCs

Endocrine

Other

10%

10%

10%

10%

10%

10%

11%

10%

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10% mervous (14%), or immune (40%) systems or because changes in their regulation would affect at least one of those systems (other.22%). B) 505 of the selectedgenes were represented by expressed sewuence tags (ESTs) in a database Zonstructed form nine blood—derived EST libraries. As expected, a large proportion of these were genes encoding 46% mmune C) PNI Genes expressed in PBMCs (26%), but genes encoding (17%) or (5%) nervous system unctions were predicted to by detectable in peripheral blood immune system proteins (52%), or classified as "other"

FIG.6-1

7/126

Category	PNI genes	Found In Blood ESTs	Expression in PBMCs
Endocrine:Hormone Metabolism	79	17	16
Hormone Receptor	95	12	18
Hormones	45	1	10
Regulated by Hormones	28	11	7
Regulates Hormone Activity	53	25	10
Regulates Hormone Expression	18	6	4
Other Neuroendocrine Function	30	12	
Nervous System: Neurotransmitter	20	0	5 3
Neurotronsmitter Metabolism	32	10	8
Neurotransmitter Receptor	100	3	27
Regulated by Neurotransmitters	2 .	1	1
Regulates Neurotransmitter Activity	51	10	13
Regulates Neurotransmitter			
Expression	1	0	0
Immune System : Apoptosis	40	26	20
Complement Component	29	7	7
Cytokine or Chemokine Receptors	90	38	28
Cytokines and Chemokines	108	31	31
MHC/HLA	18	17	4
Regulated by Cytokines or			_
chemokines	9	4	0
Regulates Cytokine Activity	20	7	3
T—cell Activation	6	3	2
Other Immune Function	261	134	79
Signal Transduction	55	31	10
Protease Inhibitor	9	4	0
Transcription Factor	92	44	16
Circadian	7	4	1
Regulation of Cell Growth	40	6	13
Growth Factor	26	5	11
Growth Factor Receptor	11	1	3
Heat shock	20	11	6
Stress Response	10	9	2
Homeostasis & Small Molecule transport	32	5	10
Other .	10	7	2
Unknown Function	4	3	4
Total	1451	505	374

FIG 6-2

<u>A</u> egCENE	negGENE	PER1	PER1	TIMELESS	TIMELESS	CSNK1	CSNK1	negGENE-B.	negGENE-B
JUC0A1	, NCOA1	POGFRB	PDGFRB	IL2RA	IL2RA	2002	S0D2	CLOCK	CLOCK
STATI	STAT1	COK4	CDK4	1GFB1	TGF81	81	81 118	FCGR1A	FCGR1A
HENC HENC	IFNG	ITGA2	ITGA2	PTGDS	PTGDS	CBP4	CBP4	VAMP2	VAMP2
AADD45B	CADD45B	ILGR	IL6R	75	CZ	E21G5	E21G5	TLR2	TLR2
DUSP14	DUSP14	2001	2001	CYP2781	CYP27B1	LAT	LAĪ	PDGFC	PDGFC
TIFIT4	IFIT4	NR:1	NR.1	S001	SOOI	CABBR1	CABBR1	NRG1	NRG1
BBCENE-B	negGENE-B	TFRC	TFRC	CABARAP	CABARAP	PER1 ANTI	PER1 ANTI	negGENE	negGENE

FIG. 7

IRETITI PARTE IN (RIII F 26)

9/126

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24														
23 2	117 37.08		129 9.62		342 41.59									
22 2	3,		6		3									
21	116 58.23		128 41.53		140 6.85									
20	1		1		- 9									
	115 59.25		127 19.18		139 10.24									
18	1		1 31		<u> </u>									
17	114 93.79		126 9.72		138 10.13									
16	6		- 6											
15	113 39.91		125 33.95		137 103.5									
14	1		3_											
	112 86.93		124 17.75		136 13.43									
11 [[12]] 13														
1	111 82.51		123 47.07		135 7.26									
10			4											
1	342 41.59		122 35.72		134 7.31									
8	†		· · · · · · · · · · · · · · · · · · ·											
7	110 22.42		121 19.05		133 17.92	343 12.26								
9	7													
5	109 39.53		120 21.14		132 7.68	344 19.64					5:03:0:00			
4	~		7			-								
3	108 27.37		119 19.45		131 6.34	142 6.86								
. 2	7													
-	343 12.26		118 52.97		130 7.54	141 41.21								
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1500 pmol	27.37	39.53	22.42	82.51	26.93	39.91	93.79	59.25	58.23	37.08	52.97	19.45	21.14	19.05	35.72	47.07	17.75	33.95	9.72	19.18	41.53	9.62	7.54	6.34
5000 pmol	91.23	131.76	74.73	275.04	89.78	133.03	312.62	197.50	194.10	123.61	176.57	64.82	70.47	63.49	119.07	156.91	59.17	113.17	32.39	63.94	138.43	32.08	25.13	21.13
∥pmol	16442.70	11384.26	20071.91	5453.72	16708.11	11275.92	4798.21	7594.94	7728.13	12135.15	8495.33	23140.64	21285.40	23624.48	12597.70	9559.51	25350.77	13254.93	46303.74	23461.13	10835.63	46755.61	29692.90	70983.45
lov	300	300	300	300	300	300	300	300	300	300	300	300	300	300	300	300	300	300	300	00£	300	300	300	300
lu/pu	1.02	0.69	1.24	0.34	1.02	0.70	0.30	0.47	0.48	9.75	0.52	1.42	18.1	1.45	0.78	65.0	1.55	0.81	2.88	1.46	89.0	2.95280	3.70616	4.39792
Mπ	54.81	37.95	66.91	18.18	55.69	37.59	15.99	25.32	25.76	40.45	28.32	77.14	70.95	78.75	41.99	31.87	84.503	44.183	154.35	78.204	36.119	155.85	198.98	236.61
8	0.36	0.23	0.43	0.12	0.34	0.26	0.11	0.17	0.18	0.26	0.19	0.45	0.45	0.46	0.57	0.20	0.27	0.14	0.50	0.26	0.12	0.51	79.0	0.73
ext coef	662300	606100	639700	660100	603300	694400	000699	963600	687100	630400	653300	579500	628600	281600	652500	640200	627200	629200	009949	654700	653400	659600	625200	616200
MM	18543	18166	18532	18472	18345	18654	18445	18522	18625	18600	18504	18421	18488	18354	18514	18629	18371	18274	18638	18657	18764	18946	18626	18587
NH2	0	0	0	0	0	0	0	0	0	0	0	0	0 .	0	0	0	0	0	0	0	0	0	0	0
mer	9	09	9	9	09	09	09	99	. 60	09	09	09	09	09	89	09	09	09	9	09	61	61	61	9
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ပ	15	25	15	17	19	10	70	12	13	12	17	17	14	16	13	14	18	24	14	15	21	11	19	21
خە	17	6	18	15	14	11	15	14	18	20.	11	18	91	14	5	22	13	12	22	23	18	20	12	12
∀	17	14	13	18	10	21	70	18	20	10	16	4	12	9	16	=	14	16	12	13	15	13	13	12
bi ogilo	PER1	TIMELESS	CSNK1	NCOA1	POGFRB	IL2RA	200S	XDOTO CFOCK	STAT1	COK4	1GFB1	611	FCGR1A	IFNG	ITGA2	SOOLA	CBP4	VAMP2	CAD045B	· IL6R	73	E21G5	TLR2	DUSP14
₽huƙs	306108	306109	306110	306111	306112	2306113	₹306114	3 06115	3 06116	306117	306118	T\$06119 ·	J06120	1306121	1306122	_306123	306124	4 306125.	=306126	TB06127	×306128°	2306129	306130	306131

FIG.9-1

11/126

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7.68	17.92	7.31	7.26	13.43	103.52	10.13	10.24	6.85	41.21	98.9	41.59	12.26	19.64	
25.59	59.74	24.36	24.21	44.77	345.05	33.77	34.14	22.85	137.36	22.86	138.65	40.88	65.46	
58607.43	25108.90	61568.87	1	33502.11	4347.16	44423.54	43935.73	65649.75	10919.86	65626.31	32456.80	36694.21	22915.65	
300	300	300	300	300	300	300	300	300	300	38	8	38	38	
3.71969	1.58515	3.89780	4.02049	2.17392	0.28092	2.97374	2.94897	4.35476	0.73123	4.38080	0.67568	2.29168	1.40617	
195.36	83.6963	205.229	206.551 4.02049	111.673 2.17392	14.4905 0.28092	148.078 2.97374	146.452 2.94897	218.832 4.35476	36.3995	218.754	36.0631 0.67568	122.314 2.29168	76.3855	
0.69	0.27	0.68	0.74	0.40	0.05	0.55	0.52	0.75	0.13	0.79	0.12	0.41	0.24	
702300	642800	008/59	720400	711000	648700	744200	703300	681800	708800	717700	005599	665500	615300	i
19040	18939	18992	19465	19467	19387	20082	20136	19900	20089	20026	18736	18736	18409	
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-61	62	62	63	63	53	සි	65	65	65	8	9	99	8	
	တ	12	13	Ξ	13	7	16	20	15	14	82	138	17	
9	24	8	23	5	19	13	14	11	5	16	7		17	
21	55	14	7	9	1	14	20	12	2	5	21	21	15	
13	7	16	23	71	=	24	15	16	11	8	7	14	Ξ	
2001	CYP27B1	LAT	POGFC	· IFIT4	NR1	SOOI	CABBR1	NRG1	TFRC	CABARAP	NEG GENE-B	NEG GENE	PER1 ANTI	
306132	396133	306134	306135	300136	306137	10 6138	306139	306140	306141	396142	397342	307343	307344	37.

FIG.9-2

SUBSTITUTE SHEET (RULE 26)

percent count crine 17.3% 65 une 46.4% 174 onal 13.9% 52 onal 13.9% 83

Gene Abbreviation	Accession #	Category	larger category
PER3	NM_016831	Circadian	other
PTGIS	NM_000961	Endocrine: Hormone Metabolism	endocrine
POR	NM_000941	Endocrine: Hormone Metabolism	endocrine
来R1C3	NM_003739	Endocrine: Hormone Metabolism	endocrine
HS01788	NM_014234	Endocrine: Hormone Metabolism	endocrine
CCP1B1	NM_000104	Endocrine: Hormone Metabolism	endocrine
CYP2S1	NM_030622	Endocrine: Hormone Metabolism	endocrine
RXAS1 vTXS-1	NM_001061	Endocrine: Hormone Metabolism	endocrine
SP4A11	NW_000778	Endocrine: Hormone Metabolism	endocrine
SP2F1	NM_000774	Endocrine: Hormone Metabolism	endocrine
JYP286	NM_000767	Endocrine: Hormone Metabolism	endocrine
77P2C8 vHp1-2	NM_030878	Endocrine: Hormone Metabolism	endocrine
24P2C8 vHp1-1	NM_000770	Endocrine: Hormone Metabolism	endocrine
*VP8B1	. NM_004391	Endocrine: Hormone Metabolism	endocrine
LDH4A1	NM_003748	Endocrine: Hormone Metabolism	endocrine
¾P2C18	NM_000772	Endocrine: Hormone Metabolism	endocrine
MP17	NM_000102	Endocrine: Hormone Metabolism	endocrine
HRB .	NM_000461	Endocrine: Hormone Receptor	- endocrine
19R2	NM_001437	Endocrine: Hormone Receptor	endocrine
39R14 · ·	NM_018949	Endocrine: Hormone Receptor	endocrine
28RMC1	NM_006667	Endocrine: Hormone Receptor	endocrine
JGR.	NM_000926	Endocrine: Hormone Receptor	endocrine
IPRI	NM_004624	Endocrine: Hormone Receptor	endocrine
ICSR	NM_005913	Endocrine: Hormone Receptor	endocrine
ara	NM_000964	Endocrine: Hormone Receptor	endocrine
ICIR	NM_002386 .	Endocrine: Hormone Receptor	endocrine
WPR1B	NM_000707	Endocrine: Hormone Receptor	endocrine

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Endocrine: R	equlates Hormone Activity	endocrine
Endocrine: R	equiates Hormone Activity	endocrine
Endocrine: R	equlates Hormone Activity	endocrine
	Endocrine: H Endocrine: R Endoc	Endocrine: Hormone Receptor Endocrine: Hormone Receptor Endocrine: Hormone Receptor Endocrine: Hormone Receptor Endocrine: Hormones Endocrine: Regulated by Hormones Endocrine: Regulates Hormone Activity

NCOA6IP	NM 024831	Endocrine: Regulates Hormone Activity	endocrine
MME v1	NM_000902	Endocrine: Regulates Hormone Activity	endocrine
CREBBP	NM_004380	Endocrine: Regulates Hormone Activity	endocrine
PCSK2	NM_002594	Endocrine: Regulates Hormone Expression	endocrine
PC v1	NM_000920	Endocrine: Regulates Hormone Expression	endocrine
IPF1	NM_000209	Endocrine: Regulates Hormone Expression	endocrine
KLK2	NM_005551	Endocrine: Regulates Hormone Expression	endocrine
NRC1vSMDF	NM_013959	Growth Factor	other
IGF1	NM_000618	Growth Factor	other
EGF	NM_001963	Growth Factor	other
TGFB3	NM_003239	Growth Factor	other
FIGF	NM_004469	Growth Factor	other
. MDK	NM_002391	Growth Factor	other
NMB	NM_021077	Growth Factor	other
PDGFA v2	NM_033023	Growth Factor	other
PDGFC	NM_016205	Growth Factor	other
PIN	NM_002825	Growth Factor	other
PDGFA v1	NM_002607	Growth Factor	other
NMBR	NM_002511	Growth Factor Receptor	other
ERBB3	NM_001982	Growth Factor Receptor	other
POGFRB	NM_002609	Growth Factor Receptor	other
HSPA9B	NM_004134	Heat shock	other
HSPB2	NM_001541	Heat shock	other
HSPB7	NM_014424	Heat shock	other
HSPA5	NM_005347	Heat shock	other
HARC	NM_017913	Heat shock	other
TRPV2	NM_016113	Heat shock	other
TRPM2	NM_003307	Homeostasis & Small Molecule transport	other
SCN5A	NM_000335	Homeostasis & Small Molecule transport	other
SCN7A	NM_002976	Homeostasis & Small Molecule transport	other
SLC15A2	NM_021082	Homeostasis & Small Molecule transport	other

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other	other	other	other	other	other	immune	immune	immune																				
Homeostasis & Small Molecule transport	Immune: Apoptosis	Immune: Complement Component	Immune: Complement Component	Immune: Complement Component																								
NM_002635	NM_080552	NM_000718	NM_004955	NM_006920	NM_006922	NM_032974	NM_033338	NM_033340	NM_018494	NM_001227	NM_033339	NM_001228	NM_003879	NM_002468	NM_003824	NM_033358	NM_014550	NM_004050	NM_033357	NM_138764	NM_0215/1	NM_033356	NM_004394	NM_006986	NM_033355	NM_139125	NM 000632	NM_000064
SLC25A3 vB	VIAAT	CACNA1B	SLC29A1	SCN1A	SCN3A	CASP10 vB	CASP7 v0	CASP7 vb	LR00 v2	CASP7 va	CASP/ vc	CASP8 vA	CFLAR	MY088	FADD	CASP8 v.	CAKU10	BCL2L2	CASP8 v0	BAX vE	CEBERG	CASP8 vC	DAP	MAGED1		MASP1 v2	II GAM	CS

immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immine	3.5
Immune: Complement Component	mmune: Complement Component	Immune: Complement Component	mmune: Complement Component	mmune: Cytokine/Chemokine Receptors	Immune: Cytokine/Chemokine Receptors	mmune: Cytokine/Chemokine Receptors	Immune: Cytokine/Chemokine Receptors	Immune: Cytokine/Chemokine Receptors	Cytokine/Chemokine Receptors	mmune: Cytokine/Chemokine Receptors	Immune: Cytokine/Chemokine Receptors																	
Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	Immune: C	
NM_000716	NM_001877	NM_001734	NM_001733	NM_003844	NM_000565	NM_148888	· NM_003842	NM_001192		NM_144701	NM_000043	NM_002183		NM_001505		NM_052962	- 11	NM_000640	***	NM_005201		NM_018725	NM_006140	NM_032871	NM_012452	NM_003841	NM_003840	
C48PB	CR2	CIS	C1R	TNFRSF10A	ILGR	CCL25 v2	TNFRSF10B v1	TNFRSF17	IL12RB2	IL-23R	TNFRSF6 v1	IL3RA	IL8RB	GPR30	CX3CR1	1L22RA2	IL22R	IL13RA2	HM74	CCR8	CCR4	IC 178R	CSF2RA v1	INFRSF19L	INFRSF13B	TNFRSF10C	INFRSF100	

L-17RC INFRSF11A L16 CCL2	007000 WN	Immune: Cytokine/Chemokine Receptors	immune
SF11A	NM_032732	Immune: Cytokine/Chemokine Receptors	immune
	NM_003839	Immune: Cytokine/Chemokine Receptors	immune
	NM_004513	Immune: Cytokines/Chemokines	immune
	NM_002982	Immune: Cytokines/Chemokines	immune
	NM_003175	Immune: Cytokines/Chemokines	immune
91	NM_022059	Immune: Cytokines/Chemokines	immune
	NM_004757	Immune: Cytokines/Chemokines	immune
NFSF12 v1	NM_003809	Immune: Cytokines/Chemokines	immune
	NM_002990	Immune: Cytokines/Chemokines	immune
	NM_003808	Immune: Cytokines/Chemokines	immune
NFSF11 v2	NM_033012	Immune: Cytokines/Chemokines	immune
	NM_000641	Immune: Cytokines/Chemokines	immune
119	NM_006274	Immune: Cytokines/Chemokines	immune
L23 v1	NM_005064	Immune: Cytokines/Chemokines	immune
30124	NM_002991	Immune: Cytokines/Chemokines	immune
CXCL13	NM_006419	Immune: Cytokines/Chemokines	immune
PAC	NM_032569	Immune: Cytokines/Chemokines	immune
	NM_021803	Immune: Cytokines/Chemokines	immune
L17F	NM_052872	Immune: Cytokines/Chemokines	immune
7.	NM_022789	Immune: Cytokines/Chemokines	immune
0.11	NM_005409	Immune: Cytokines/Chemokines	immune
CL 10	NM_001565	Immune: Cytokines/Chemokines	immune
CCL16	NM_004590	Immune: Cytokines/Chemokines	immune
CL13	NM_005408	Immune: Cytokines/Chemokines	immune
	NM_002981	Immune: Cytokines/Chemokines	immune
4	XM_170924	Immune: Cytokines/Chemokines	immune
1F8	NM_014438	Immune: Cytokines/Chemokines	immune
יון	NM_002995	Immune: Cytokines/Chemokines	immune
3	NM_002188	Immune: Cytokines/Chemokines	immune
L1F9	NM_019618	Immune: Cytokines/Chemokines	immune

immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune
Immune: Cytokines/Chemokines	Immune: Cytokines/Chemokines	Immune: Cytokines/Chemokines	mmune: MHC/HLA	Immune: MHC/HLA	Immune: MHC/HLA	Immune: MHC/HLA	Immune: Other Immune Function	mmune: Other Immune Function	Immune: Other Immune Function	Immune: Other Immune Function	Immune: Other Immune Function	mmune: Other Immune Function	mmune: Other Immune Function	Immune: Other Immune Function	Immune: Other Immune Function	Immune: Other Immune Function	mmune: Other Immune Function	mmune: Other Immune Function	mmune: Other Immune Function	Immune: Other Immune Function	Immune: Other Immune Function	Immune: Other Immune Function	mmune: Other Immune Function						
NM_000588		NM_003680 Im		NM_033554 Im	NM_021983				NM_013254 . Im		NM_002462 Im	NM_006435 Im	NM_004960 Im	NM_003641 Im		NM_002262 Im	NM_000201 Im		NM_053282 Im		NM_130848 Im	(NM_000061 Im		NM_024013 (Im	NM_000605 lm		NM_021002 Im	NM_005755 Im
IL3 NM_(OSIMR NM_(YARS	HLA-A NM_(HLA-DPA1 · NM_(HLA-DRB4 NM_(MHC2TA NM_(TBK1 NW_(A	•	IFITM2 · NM_(FUS NM_(FITM1 NM_(' v1	KLRD1 v1 NM_(ICAM1 NM_(HRH1 NM_(EAT2 NM_(CYSLTR1 NM_(DCNP1 NM_	FCGR3A NM_(l			IFNA4 NM_(IFNA6 NM_(EBI3 NM_(

FNGR1	NM 000416	Immine: Other Immine Finction	immine
TGAL	NM_002209	Immune: Other Immune Function	immune
FCGR1A	NW_000566	Immune: Other Immune Function	immune
PRV1	NM_020406	Immune: Other Immune Function	immune
TGAX	NM_000887	200	immune
AIM2	NM_004833	Immune: Other Immune Function	immune
CO1E	NM_030893	Immune: Other Immune Function	immune
:030	NM_000732	Immune: Other Immune Function	immune
CD8A	NM_001768	Immune: Other Immune Function	immune
EAF1	NM_033083	Immune: Other Immune Function	immune
F116	NM_005531	Immune: Other Immune Function	immune
CD3Z	NM_000734	Immune: Other Immune Function	immune
FNGR2	NM_005534	Immune: Other Immune Function	immune
FCGR3B	NM_000570	Immune: Other Immune Function	immune
[R2	NM_003264		immune
RIM	NM_016388	Immune: Other Immune Function	immune
PLA264A	NM_024420	Immune: Other Immune Function	immune
PTGER3	NM_000957	Immune: Other Immune Function	immune
PTGER4	NM_000958	Immune: Other Immune Function	immune
HAVCR2	NM_032782	Immune: Other Immune Function	immune
PTPN9	NM_002833	Immune: Other Immune Function	immune
FCER1G	NM_004106	Immune: Other Immune Function	immune
	NM_080589	Immune: Other Immune Function	immune
PTPN7 v2	NM_080588	Immune: Other Immune Function	immune.
FNA14	NM_002172	Immune: Other Immune Function	immune
ADA	NM_000022	Immune: Other Immune Function	immune '
RelA	NM_021975		immune
ILR1	NM_003263	Immune: Other Immune Function	immune
IPT1	NM_003295		immune
TLR10	NM_030956	Immune: Other Immune Function	immune

immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune	immune						
Immune: Other Immune Function	mmune: Other Immune Function	mmune: Other Immune Function	mmune: Other Immune Function	Immune: Regulates Cytokine Activity	Immune: Regulates Cytokine Activity	Immune: Regulates Cytokine Activity	Immune: T-cell Activation																						
Immi	lmmı	Imm	lmm	lmm	Imm	lmm	Imm	Imm	lmm	Imm	lmm	Imm	Imm	lmm	Imm.	Imm	Imm	Imm	Immr	Imm	lmm	lmm	lmm	lmm	lmm	lmmu	lmm	lmm	Imm
NM_004470	NM_057092	NM_000801	NM_054014	NM_003255	NM_138296	NM_002832	NM_002108	NM_002460	NM_003177	NM_000960	NM_022718	NM_138738	NM_014387	NM_004705	NM_012092	NM_005533	NM_007161	NM_021706	NM_021708	NM_002421	NM_004895	NM_001925	NM_002175	NM_002173	NM_002287	NM_004899	NM_006068	NM_016509	INM_017/43
FKBP2 v1	FKBP2 v2	FKBP1A v12B	FKBP1A v12A	TIMP2	PICRA	PTPN7 v1	HAL	IRF4	SYK	PTGIR	MMP25	SPAP1	IAI	PRKRIR	1005	IF135			LAIR1 vD	MMP1	CIASI	DEFA4	IFNA21	IFNA16	LAIR1 vA	BRE	ILK6	CLECZ	UPP8 v2

0PP8 v1	NM_130434	Immune: T-cell Activation	immune
PNOC	NM_006228	Neuronal: Neurotransmitter	neuronal
TAC3	NM_013251	Neuronal: Neurotransmitter	neuronal
NPPA	NM_006172	Neuronal: Neurotransmitter	neuronal
MAOA	NM_000240	Neuronal: Neurotransmitter Metabolism	· neuronal
严	NM_000360	Neuronal: Neurotransmitter Metabolism	neuronal
COMT VMB	NM_000754	Neuronal: Neurotransmitter Metabolism	neuronal
COMT vS	NM_007310	Neuronal: Neurotransmitter Metabolism	neuronal
NAALAD2	NM_005467	Neuronal: Neurotransmitter Metabolism	neuronal
PC v2	NM_022172	Neuronal: Neurotransmitter Metabolism —	neuronal
BB0X1	NM_003986	Neuronal: Neurotransmitter Metabolism	neuronal
RNPEPL 1	NM_018226	Neuronal: Neurotransmitter Metabolism	neuronal
TACR2	NM_001057	Neuronal: Neurotransmitter Receptor	neuronal
CHRNA9	NM_017581	Neuronal: Neurotransmitter Receptor	neuronal
CHRNA6	NM_004198	Neuronal: Neurotransmitter Receptor	neuronal
CHRNB4	NM_000750	Neuronal: Neurotransmitter Receptor	neuronal
CHRNB2	NM_000748	Neuronal: Neurotransmitter Receptor	neuronal
NPR2 VL	NM_003995	Neuronal: Neurotransmitter Receptor	neuronal
ADRA1A v2	NM_033303	Neuronal: Neurotransmitter Receptor	neuronal
HTR5A	NM_024012	Neuronal: Neurotransmitter Receptor	neuronal
GABRG3	NM_033223	Neuronal: Neurotransmitter Receptor	neuronal
DRD4	NM_000797	Neuronal: Neurotransmitter Receptor	neuronal
CHRNB3	NM_000749	Neuronal: Neurotransmitter Receptor	neuronal
NPY1R	606000 MN	Neuronal: Neurotransmitter Receptor	neuronal
CABRR1	NM_002042	Neuronal: Neurotransmitter Receptor	neuronal
CABBR1 v2	NM_021903	Neuronal: Neurotransmitter Receptor	neuronal
CABBR1 v3	NM_021904	Neuronal: Neurotransmitter Receptor	neuronal
GRIA3 vFlip	NM_007325	Neuronal: Neurotransmitter Receptor	neuronal
GRIA1 vFlop	NM_000827	Neuronal: Neurotransmitter Receptor	neuronal
GRIA3 vFlop	NM_000828	Neuronal: Neurotransmitter Receptor	neuronal

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CABRE v3	NM_021987	Neuronal: Neurotransmitter Receptor	neuronal
CABRA3	NM_000808	Neuronal: Neurotransmitter Receptor	neuronal
GRM8	NM_000845	Neuronal: Neurotransmitter Receptor	neuronal
GRM7	NM_000844	Neuronal: Neurotransmitter Receptor	neuronal
GRM4	NM_000841	Neuronal: Neurotransmitter Receptor	neuronal .
CABRQ	NM_018558	Neuronal: Neurotransmitter Receptor	neuronal
HTR4	NM_000870	Neuronal: Neurotransmitter Receptor	neuronal
NPR2 vS	NM_000907	Neuronal: Neurotransmitter Receptor	neuronal
Tar1	NM_138327	Neuronal: Neurotransmitter Receptor	neuronal
ADG-90	NM_033069	Neuronal: Regulated by Neurotransmitters	neuronal
180	NM_020548	Neuronal: Regulates Neurotransmitter Activity	neuronal
CDV-1	NM_031473	Neuronal: Regulates Neurotransmitter Activity	neuronal
ADRA2C	NM_000683	Neuronal: Regulates Neurotransmitter Activity	neuronal
KLF16	NM_031918	Neuronal: Regulates Neurotransmitter Activity	neuronal
SLC1A1	NM_004170	Neuronal: Regulates Neurotransmitter Activity	neuronal
ARIX	NM_005169	Neuronal: Regulates Neurotransmitter Activity	neuronal
SLC25A20	NM_000387	Neuronal: Regulates Neurotransmitter Activity	neuronal
NTT73	NM_018057	Neuronal: Regulates Neurotransmitter Activity	neuronal
SYN2 v lia	NM_133625	Neuronal: Regulates Neurotransmitter Activity	neuronal
NTTS	NM_014037	Neuronal: Regulates Neurotransmitter Activity	neuronal
CONF	NM_000514	Neuronal: Regulates Neurotransmitter Activity	neuronal
PPP1R1B	NM_032192	Neuronal: Regulates Neurotransmitter Activity	neuronal
ADRBK1	NM_001619	Neuronal: Regulates Neurotransmitter Activity	neuronal
F3	NM_001993	Other	other
TIMM23	NM_006327	Other	other
2002	NM_003469	Other Neuroendocrine Function	other
INSM1	NM_002196	Other Neuroendocrine Function	other
RTN3	NM_006054	Other Neuroendocrine Function	other
SCGB1A1	NM_003357	Other Neuroendocrine Function	other

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SYP	XM_028505	Other Neuroendocrine Function	other
IGFBP3 ·	NM_000598	Regulation of Cell Growth	other
PTCH	NM_000264	Regulation of Cell Growth	other
WNT2	NM_003391	Regulation of Cell Growth	other
NRG1 vGGF2	NM_013962	Regulation of Cell Growth	other
COK4 v2	NM_052984	Regulation of Cell Growth	other
MTIH	NM_005951	Cell Growth	other
IGFBP5	NW_000599	Regulation of Cell Growth	other
PRSS1-1	NM_002775	Cell Growth	other
NGFRAP1	NM_014380	Regulation of Cell Growth	other
GFRA2	NM_001495	Cell Growth	other -
MTZA	NM_005953	Regulation of Cell Growth	other
ICFBP2	NM_000597	Cell Growth	other
NIF3	NM_002527	Regulation of Cell Growth	other
ICK	NW_005356		other
SCAP1	NM_003726	Signal Transduction	other
AIP	NM_003977	Transduction	other
MAP3K8	NM_005204	Signal Transduction	other
TEC	NM_003215	Transduction	other
GFRA3	NM_001496	Signal Transduction	other
RAF1	NM_002880	Transduction	other
MAPKI	NM_002745	Signal Transduction	other
PRKCE	NM_005400		other
PRKCB1	NM_002738	Signal Transduction	other .
NR1	NM_014434		other
S002	NM_000636	Stress Response	other
6101-3	NM_016265	Transcription Factor	other
STAT5B	NM_012448	Transcription Factor	other
STAT3 vi	NM_139276	Transcription Factor	other

GIOT-2	NM_016264	Transcription Factor	other
ZNF14	NM_021030	Transcription Factor	other
EN2	NM_001427	Transcription Factor	other
TCF8	1 1	Transcription Factor	other
MDM2 vA	. ,	Transcription Factor	other
STAT3 v2		Transcription Factor	other
CEBPG		Transcription Factor	other
GATA3 .	NM_002051	Transcription Factor	other
NMI	NM_004688	Transcription Factor	ofher
RFX2 v1	NM_000635	Transcription Factor	other
IRF5 v1	NM_002200	Transcription Factor	other
RFX2 v2	NM_134433	Transcription Factor	ofher
IRF3	NM_001571	Transcription Factor	other
NFKBIL2		Unknown Function	other
WSB1 v2	NM_134265	Unknown Function	other
PTPN18	NM_014369	Unknown Function	other
WSB1 v1	NM_015626	Unknown Function	other

FIG.10-13

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JJ 1906	26.7	23.33	23.04	20.24	22.87	22.87	22.87	22.87	17.44	14.82	14.82	21.5	11.91	17.64	16.21	21.1	19.07	19.07	13.09	13.09	15.82	17.02	21.64	60.9	4.85	16.14	10.39	8.83		8.83
JJ 8861	27.37	21.25	21.67	12.36	22.06	22.06	22.06	22.06	17.58	10.73	10.73	21.28	7.87	13.26	18.33	14.13	15.92	15.92	8.19	8.19	15.79	18.17	18.33	4.57	4.53	13.12	7.65	6.36	6.36	6.36
JJ 9479	104.65	69.17	61.85	63.51	41.47	41.47	41.47	41.47	23.91	25.06	25.06	32.63	28.34	37.71	36.49	35.38	33.27	33.27	32.02	32.02	14.72	27.69	42.38	7.13	16.3	28.95	22.18	21.66	21.66	21.66
JU 9315	71.73	76.33	43.79	47.94	45.97	45.97	45.97	45.97	39.87	30.68	30.68	41.18	36.2	25.85	22.97	17.15	17.74	17.74	32.75	32.75	24.09	21.61	21.04	17.55	11.06	25.66	20.49	22.06	22.06	22.06
JJ 8219	62.76	64.71	58.2	27.46	42.64	42.64	42.64	42.64	38.63	19.37	19.37	39.84	19.12	40.14	31.01	24.9	25.33	25.33	20.49	20.49	22.3	22.32	23.79	29.68	14.44	33.24	12.6	13.85	13.85	13.85
Gene Abbreviation	GNRH2	MT3	E21G2	GRIA3 vFlop	SCN2B	SCN2B	SCN2B	SCN2B	HK2	L11	MHC2TA	B7-H3	GPR81	BCL2L1 v1	0001	NPFF	HSPA1A	HSPA1B	MT1H	MT2A	WNT10B	SLC21A2	TMSB4X	ALDH1A2	NMB	FIT4	CXCL16	BAX vE	CASP8 vA	CASP8 vB
ove ·	83.23833333 (68.7794444	-	46.25722222	46.04111111	46.04111111	46.04111111	46.0411111	40.46611111	39.24277778	39.24277778	38.16166667	37.27611111	34.74888889	33.90888889	29.4744444	29.39833333			_	28.21166667	28.0255556	27.127778	26.05888889	25.97	25.72111111	24.53333333	20.63722222	20.63722222	20.63722222
	ш	_			_	Ц		L	ئــــا	Ц		L	ـــــا	Щ.	Щ.	Ц	لــــــا	Ц			L		L	i	L	L	L	_	L	ш.

1,0,7295 W 202597 W 203445 W 203215 W 204118 W 202431 PIF 20 1,0,7295 W 202597 W 203445 W 20315 W 203597 W 202431 PIF 20 1,05,74 50,43 40,96 49,13 80,11 62,75 32,14 111 1,05,74 50,59 37,18 53,18 41,68 49,17 35,71 49,17 1,0,31 59 52,22 50,45 68,56 68,12 31,66 88 1,0,45 57,59 37,18 53,18 41,68 49,17 35,71 49,17 49,27 42,28 49,17 35,23 29,23 35,23 29,23 35,23 29,23 35,23 29,23 35,23 36,23 </th <th></th> <th></th> <th></th> <th>-</th> <th></th> <th>_</th> <th>_</th> <th></th> <th>~ ·</th> <th></th> <th></th> <th></th> <th>_</th> <th></th>				-																			_	_		~ ·				_	
10.725 W 202597 W 202415 W 204315 W 204315 W 204315 W 204315 W 204311 W 204311 158.53 16.63 11.64 11.044 13.31 10.48 11.64 11.044 13.31 10.48 11.48 11.044 13.31 10.48 11.48 11.044 13.31 10.48 11.044 13.31 10.48 10.48 10.44 10.44 13.31 10.48 10.44 10.44 13.31 10.48 10.44 10.53 <td>2</td> <td>3.44</td> <td>8.</td> <td>3.47</td> <td>36.</td> <td>3.96</td> <td>9.6</td> <td>9.96</td> <td>9.6</td> <td>5.7.</td> <td>4.3</td> <td>4.3</td> <td>6.61</td> <td>0.0</td> <td>3.28</td> <td>35.8</td> <td>4.51</td> <td>30.8</td> <td>30.8</td> <td>0.7</td> <td>0.7'</td> <td>3.9(</td> <td>0.19</td> <td>4.49</td> <td>0.35</td> <td>37.</td> <td>24.(</td> <td>6.7.</td> <td>12.9</td> <td>12.0</td> <td>12.0</td>	2	3.44	8.	3.47	36.	3.96	9.6	9.96	9.6	5.7.	4.3	4.3	6.61	0.0	3.28	35.8	4.51	30.8	30.8	0.7	0.7'	3.9(0.19	4.49	0.35	37.	24.(6.7.	12.9	12.0	12.0
108.795 W 202597 W 203455 W 203455 W 203455 W 203455 W 203457 W 203451 W 203457 PIF 2167 PIF 2177 PIF 2167 PIF 2167 PIF 2167 PIF 2167 PIF 2167 PIF 2168		33	7	<u>}9</u>	5	3(3	3	3	5	4	4	3	3	بر		7		,	3	3	3	يم	7	4	Ĭ		3			
158.29 W 20245 W 20345 W 20345 W 20345 W 20345 W 20345 W 20345 P 2035 H 2035	PF																														
158.29 W 20245 W 20345 W 20345 W 20345 W 20345 W 20345 W 20345 P 2035 H 2035	-	-	-	53	55	.3	3	13	3	77	72	12	33	65	12	7	17	.2	.2	14	14	17	19/	65	37	79	79)2	99	99	9
158.29 W 20245 W 20345 W 20345 W 20345 W 20345 W 20345 W 20345 P 2035 H 2035	113	4.8	30.3	32.3	39.6	75.2	75.2	75.2	75.2	15.7	14.7	14.7	37.5	39.E	10. 4	35.5	33.3	27	27	30.4	30.4	12.1	38.7	17.6	37.8	39.7	24.7	35.(30.9	33	8
10.58.59 G.4.29 G.5.51 W 202373 W 202437 W 202437 W 202437 W 202437 W 202437 PIF 2057 PIF 2127 PIF 2052 PIF 2168 PIF 217 PIF 2052 PIF 217 PIF 2053 PIF 2053 PIF 2053 PIF 2053 PIF 2053 PIF 2053 PIF 2054 P		13		"	3)	, _		•		,	,	7			7		•••			. ,	. 1	,		Ì			,				
10.7295 W 20255/W 202545 W 204373 W 204373 W 204373 W 204373 P 20257 P F 2027	Ы																														
10.7295 W 20255/W 202545 W 204373 W 204373 W 204373 W 204373 P 20257 P F 2027	30	83	.31	.65	.84	.14	.14	.14	.14	.98	.51	.51	.24	.14	.23	.32	0.1	.85	.85	.29	.29	.34	1.4	98.	.78	.54	81	.84	.42	.42	.42
158.259 W 20255/F W 20345 W 204313 W 20418 W 202431 PIF 2057 PIF 2052 PIF 2053 PIF 2052	216	16	73	67	22	57	57	57	57	63	9	10	34	31	48	44	3	32	32	31	31	45	4	27	53	56	70	32	တ	တ	တ
10.7255 W 202597 W 203215 W 204373 W 204118 W 202431 PIF 2057 PIF 2052 PIF 2057 PIF 2052 PIF 2057	능																														
10.7295 W 20259T W 20245 W 20215 W 20437 W 204118 W 202431 PIF 207 PIF 217		3	4	6	7	6	6	9	6	-	2	5	4	8	2	2	7	1	1	4	4	2	3	5	ļ	_	6	9	8	8	82
10.7295 W 202597 W 20345 W 202515 W 204373 W 20418 W 202431 IF 2057 IF 2127 IF 11)52	8.8	0.4	0.6	5.8	59.	59.	59	59	8.3	0.8	0.8	6.1	3.1	4.8	3.9	3.2	3.3	.3.3	0.9	0.9	1.1	1.9	9.9	1.8	9.4	12	25.	5.7	5.7	5.7
10.7295 W 202597 W 20245 W 20215 W 204373 W 204313 PIF 2057 PIF 2127 110.31 56.51 41.32 62.05 64.87 34.56 126.87 118.11 105.74 50.43 40.13 62.05 64.87 34.56 126.87 118.11 105.74 50.43 40.96 49.13 62.05 32.14 111.76 114.3 107.45 57.59 37.18 62.86 53.23 29.23 32.86 51.98 58.47 44.63 46.27 41.97 62.86 53.23 29.23 32.86 51.98 58.47 44.63 46.27 41.97 62.86 53.23 29.23 32.86 51.98 58.47 44.63 46.27 41.97 62.86 53.23 29.23 32.86 51.98 58.47 44.63 46.27 41.97 62.86 53.23 29.23 32.86 51.98 58.47 44.63 46.27 41.97		15	11	4	-					7	9	9	5	9	7	3	4	4	4	4	7	2	~>	7	ر ع	כא					
158.59 W 202597 W 202455 W 202457 W 202457 W 202457 PIF 2057 <	늅																														
158.59 W 202597 W 202455 W 202457 W 202457 W 202457 PIF 2057 <	1	11	1.3	75	63	98	98	98	88	5.4	41	41	43	05	58	3.1	03	13	13	97	97	.03	83	64	25	81	56	24	49	49	49
158.59 W 202597 W 202455 W 202457 W 202457 W 202457 PIF 2057 <	212	₩.	117	63.	70.	51.	51.	51.	51.	õ	77.	77.	42.	35.	34.	3	26.	32.	32.	37.	37.	47.	45	30.	54.	45	22	31.	32.	32.	32
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LINGURGITUTE CHEET (RIII F)61	二	<u> </u>	L	<u></u>		L		2	Ш	bo	L7	II		口	<u> </u>	R	4	<u> </u>	-	7	⊅ा	Ή	F	5	<u>'</u> ਨ	-	L	L	ـــــ		<u></u>

FIG.11-1B

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6.36	6.36	7.18	7.18	6.54	3.22	3.22	14.07	8.49	10.69	9.61	90.9	9.89	3.87	4.71	10.66	14.62	3.29	8.9	16.21	16.21	16.21	15.79	9.4	10.51	10.51	10.51	6.11	4.1
21.66	21.66	24.44	24.44	3.63	7.53	7.53	18.49	16.66	6.03	20.3	12.27	11.07	13.61	9.62	22.85	26.41	12.49	18.09	22.89	22.89	22.89	21.73	10.22	17.15	17.15	17.15	8.47	9.7
22.06	22.06	20.19	20.19	16.04	14.03	14.03	8.27	21.09	13.18	16.39	14.91	17.11	20.37	13.34	11.59	16.11	12.37	4.43	11.64	11.64	11.64	10.06	9.42	10.54	10.54	10.54	15.01	18.97
13.85	13.85	8.95	8.95	15.43	21.26	21.26	11.56	21.76	16.23	18.93	16.78	15.05	10.49	22.7	17.95	17.43	7.67	6.54	10.79	10.79	10.79	90.6	14.44	12.25	12.25	12.25	9.44	-19.65
20.63722222 CASP8 vC	20.63722222 [CASP8 vD		20.095 ITGAL	19.60611111 C7	17.78388889 SNX15 vA	17.78388889 SNX15 VB	16.50388889 WAS		15.75388889 NPPB	15.385 ICFBP4	14.88388889 ICAM1	14.83166667 CADD45C	14.64888899 INFRSF10B v1	13.90888889 APOE	13.59888889 PTCH	12.95166667 [CHRNB1	12.945 ADRA1A v2	12.65111111 L18	12.3333333 GFRA4 v1	12.3333333 GFRA4 v2	12.3333333 GFRA4 v3	12.21833333 C10A	12.09722222 SYK	12.07333333 CXCL1	12.0733333 CXCL2	12.07333333 CXCL3	11.77333333 NIF3	11.38142857 ITGAX

3003	12.9	12.9	13.71	13.71	34.12	33.24	33.24	17.8	13.06	22.57	11.95	12.2	20.53	12.55	19.23	2.81	5.97	14.87	12.96	12.93	12.93	12.93	14.25	14.51	11.26	11.26	11.26	13.59	
出																													
PF 2113	30.96	30.96	33.22	33.22	42.69	24.55	24.55	21.24	14.84	16.55	12.72	22.95	17.42	14.98	9.97	2.33	5.78	18.52	12.05	7.76	7.76	7.76	15.79	8.03	9.51	9.51	9.51	11.72	5.94
PIF 2160	9.45	9.42	28.03	28.03	27.71	36.79	36.79	22.03	12.93	27.37	14.02	13.46	19.34	14.91			7.55	16	13.15	11.63	11.63	11.63	16.23	14.83	11.47	11.47	11.47	8.15	3.04
PIF 2052	5.78	5.78	17.75	17.75	24.53		23.13		13.09	19.92	11.26	13.58	13.88	13.18	7.42	1.65	6.8	22.72	11.59	10.53	10.53	10.53	12.86	6.41	11.73	`11.73	11.73	17.23	12.71
PIF 2127	32.49	32.49	12.43		41.68		40.26		13.72	22.6	10.2	16.21	23.7	11.36	12.65	3.83	5.68	18.55	9.26	10.12	10.12	10.12	12.22	12.61	10.62	10.62	10.62	19.21	4.14
PIF 2057	10.7	10.7	26.43	26.43	36.43	27.26	27.26	16.21	10.3	16.27	14.32	29.73	15.25	13.86	8.62	2.19	5.26	16.82	12.17	10.34	10.34	10.34	9.08	9.25	18.58	18.58	18.58	14.88	8.31
W 202431	20.34	20.34	20.45	20.45	10.54	8.01	8.01	19.73	13.25	11.92	11.75	10.07	10.1	16.19	17.01	21.66	13.11	8.04	19.42	11.19	11.19	11.19	9.67	13.35	9.81	9.81	9.81		
W 204118	32.55	32.55	22.68	22.68	15.67	12.07	12.07	11.81	18.58	14.64	17.66	14.63	16.21	17.1	11.11	12.6	15.33	15.53	8.16	14.02	14.02	14.02	11.14	10.28	8.81	8.81	8.81	13.83	18.35
W 204373	25.74	25.74	22.28	22.28	19.48	13.07	13.07	10.6	13.55	17.73	13.09	12.61	17.43	18.76	13.42	13.93	12.31	12.6	11.21	15.92	15.92	15.92	10.78	9.03	7.18	7.18	7.18	12.22	14.34
W 203215	22.82	22.82	17.82	17.82	16.87	14.86	14.86	10.15	17.97	14	18.39	15.88	15.72	14.6	17.13	14.88	16.19	11.81	7.08	10.98	10.98	10.98	9.16	13.63	13.66	13.66	13.66	13.25	13.38
W 203445	41.87	41.87	. 26.67	26.67	11.86	12.29	12.29	23.53	19.8	16.81	17.11	14.63	11.81	26.09	25.13	33.41	13.81	12.65	27.82	10.85	10.85	10.85	10.77	21.82	13.83	13.83	13.83		
W 202597	31.58	31.58	34.78	34.78	10.09	11.07	11.07	32.91	20.32	17.66	14.66	10.96	13.23	17.37	20.65	41.82	13.01	13.66	32.41	13.92	13.92	13.92	9.5	18.62	11.4	11.4	11.4		
17295	21.56	21.56	13.97	13.97	11.75	13.68	13.68	7.44	34.75	7.42	35.76	23.16	8.54	17.47	20.78	13.66	.24.53	10.4	6.78	8.59	8.59	8.59	10.01	13.01	21.38	21.38	21.38	4.81	20.78

FIG.11-2B

	L								I											ł				L					-	_
11.43	10.42	6.54	11.15	4.92	17.88	23.05	7.34	20.93	5.95	3.64	5.64	4.66	3.13	11.5	5.11	17.11	6.14	10.29	6.43	5.67	16.37	16.37	15.02	5.9	8.34	14.7	9.43	8.21	8.21	8.21
16.68	7.79	6.92	5.96	5.64	4.31	8.62	1.87	3.28	14.98	5.93	6.34	4.61	7.65	3.6	8.08	6.53	2.75	5.03	14.96	3.13	2.26	2.26	7.66	4.13	5.74	4.14	1.23	3.98	3.98	3.98
12.38	4.98	6.17	5.81	4.86	4.86	7.29	3.02	1.23	14.63	11.31	6.3	4.21	9.79	3.07	8.99	6.09	2.55	3.91	15.93	1.81	1.63	1.63	9.49	3.7	5.55	5.13	1.99	3.88	3.88	3.88
12.37	7.02	7.28	11.68	12.54	9.86	7.25	4.24	7.9	19.35	7.62	10.99	1.17	3.47	11.54	3.12	14.09	4.19	5.19	5.66	1.79	2.96	2.96	11.08	5.53	11.4	6.21	4.59	5.52	5.52	5.52
11.92	5.89	6.83	10.15	6.54	13.16	-10.89	5.9	15.04	6.31	7.08	8.89	5.91	8.05	9.99	7.81	10.1	3.18	6.39	6.87	8.67	10.25	10.25	8.47	4.94	7.26	3.5	8.85	6.83	6.83	6.89
13.28	10.13	10.88	14.35	4.1	14.31	11.7	5.95	20.67	5.01	3.33	7.62	6.29	7.55	13.64	8.72	10.74	6.34	9.84	6.73	9.03	10.93	10.93	1.76	7.11	7.25	8.33	11.62	5.89	5.89	5.89
TCF4	ENSA	TNFRSF6B vM68E		IL-23R	TLOC1	GPR50	CD44	HSPA6	CEBPB			CHGA	ABCB1	RELB	CLC	CHRNA10	SNAP25 v2	11.1F9	2002	NFKBIA	COMT VMB	COMT vS	ADRA18	HARC	SCYA3	CACNG2	RAI .	artn vi	artn v2	ARTN v3
10.93722222	10.80833333	10.7477778	9	10.32277778	10.04166667	10.03764706	9.89722222	9.871666667	9.546666667	9.263333333	9.225	8.93777778	8.90944444	8.655882353	8.546666667	8.52222222	8.306470588	8.27	5	8.130555556	7.913888889	7.913888889	7.911176471	7.780555556	7.776111111	വ	7.57722222	7.463333333		7.463333333

FIG.11-3A

4.16	9.72	15.13	12.98	16.03	6.83	5.84	17.57	3.31	7.96	7.86	13.85	18.58	9.63	8,33	11.22	7.22	21.1	9.86	3.82	14.43	7.22	7.22	7.28	12.61	9.91	11.18	9.52	5.97	5.97	5 97
3.48	6.46	13.36	6.82	17.17	5.59	6.8	22.84	2.19	90.6	14.41	11.16	18.51	12.93	3.74	7.9	5.48	10.7	7.48	3.72	8.37	6.33	6.33	5.79	15.86	8.26	8.13	6.57	20.6	20.6	306
3.47	8.12	12.36	10.32	10.47	6.39	17.51	14.39	3.17	12.17	16.98	14.17	15.93	8.06	3.88	10.85	8.83	20.41	5.79	4.99	12.23	10.65	10.65	9.26	10.44	9.7	10.86	7.78	11.47	11.47	111/7
4.12	5.68	11.44	5.06	10.78	6.99	8.8	15.25	1.21	12.88	18.71	13.86	14.78	11.48	5.4	8.63	5.88	7.74	12.05	7.47	13.83	11.12	11.12	4.68	12.41	8.88	11.65	4.38	99'.	7.66	766
4.07	9.06	13.1	9.79	7.02	6.84	6.61	20.29	5.6	9.22	11.41	10.43	. 24.1	15.24	3.37	12.52	5.93	18.43	8.35	5.93	12.85	11.3	11.3	5.78	13.99	7.1	10.33	10.33	8.57	8.57	Q 5.7
3.57	10.7	10.22	8.35	11.05	8.75	10.88	19.22	2.24	5.51	7.17	10.61	11.43	9.35	4.07	10.41	7.14	13.29	10.28	3.52	13.8	7.73	7.73	4.89	14.9	တ	10.59	4.45	5.61	5.61	5.61
17.17	16.32	11.39	13.94	13.1	13.75	6.71	7.1	12.36	8.34	4,13	5.05	5.37	9.48	10.07	7.69	9.9	5.72	8.12	13.18	4.38	3.35	3.35	6.39	4.21	7.17	3.69	9.37	6.61	6.61	12.2
11.43	10.34	8.77	9.02	80.6	99.7	12.87	4.76	21.05	6.89	7.09	10.59	4.52	6.74	11.85	6.52	9.71	2.72	5.86	5.29	7.25	3.89	3.89		3.83	6.82	7.53	9.17	6.84	6.84	78 9
10.69	11.16	12.2	7.68	10.44	7.37	8.76	5.94	17.11	7.52	23.19	11.48	5.72	8.12	10.86	8.04	7.37	3.15	7.57	7.04	6.58	8.14	8.14	5.56	3.86	7.47	6.17	8.55	5.17	5.17	5 17
5.84	10.24	8.45	11.31	90.9	11.84		5.52	17.85	5.42	5.04	8.36	5.97	7.91		8.48	9.71		9.95	6.62	10.49	10.26	10.26	9.95	4.77	6.03	8.34	10.79	5.01	5.01	5.01
25.2	20.79	13.58	22.45	24.83	22	7.34	7.69	16.26	9.91	4.51	5.13	5.3	10.11	17.55	10.94	8.15	6.17	10.95	16.57	6.7	7.29	7.29	7.47	5.76	7.51	3.88	9.24	8.04	8.04	800
25.61	. 29.73	18.84	13.98	11.16	12.3	9.72	9.76	9.29	10.73	7.33	5.58	3.82	11.68	14.69	8.81	6.72	6.63	11.95	11.97	5.34	10.77	10.77	7.66	.6.1	6.58	3.34	8.53	8.42	8.42	C7 X

FIG.11-3B

				=	—	-	_		,				_		_		1											
8.21	6.38	8.64	6.4	1.98	7.29	3.15	3.15	15.32	4.57	12.81	3.75	8.8	8.8	3.81	3.96	2.06	2.06	5.59	5.53	3.51	2.26	8.49	11.22	4.77	7.5	2.82	2.82	4.31
3.98	2.02	4.64	2.91	5.21	2.71	8.24	8.24	6.65	3.44	3.54	10.39	5.23	5.23	8.7	9.35	0.75	0.75	9.33	8.65	3.26	2.48	2.41	0.92	2.59	4.52	6.11	6.11	9.67
3.88	1.23	2.97	2.84	5.86	2.19	6.4	6.4	7.01	3.73	4.82	8.03	6.63	6.63	4.92	7.98	-	-	10.18	7.51	2.86	1.76	2.52	0.8	1.92	6.33	<u></u>	8	10.52
5.52	4.17	7.91	6.18	4.8	6.21	6.16	6.16	9.52	7.06	12.03	6.26	12.08	12.08	3.03	4.15	1.67	1.67	3.81	4.09	4.48	15.65	6.11	1.77	<u></u>	9.95	4.93	4.93	9.19
6.89	11.73	2.81	5.25	3.51	7.41	3.28	3.28	9.38	4.51	96.9	3.86	5.95	5.95	3.14	5.48	1.4	1.4	7.21	2.39	5.37	2.12	6.09	6.16	6.2	5.28	3.63	3.63	5.55
5.89	98.9	6.43	5.53	2.37	7.64	3.82	3.82	9.13	3.85	7.61	5.26	5.36	5.36	4.44	5.76	1.22	1.22	7.95	4.3	5.38	1.61	9.9	7.63	3.23	4.63	4.6	4.6	5.55
ARIN v4	CC_13	SLC6A12		SLC6A3	IL21R	LTB v1	LTB v2	CD2	CCL4	ADRA1A v4	MS4A4A v1	MAPKAPK2 v1	MAPKAPK2 v2		CLEC2	ILTIRA vi	IL11RA v2	INFRSF5 v1	CDKN1A	VIAAT	ARIX	PRKCB1	PPARD	CASP7 vb	FOS	SP110	SP110 vC	CTF1
	7.383888889	7.28777778		6.943888889	6.87944444	6.843888889	6.843888889	6.70277778	2	\neg	6.39555556	6.391111111	6.391111111	5		6.12444444	6.12444444	6.08777778					∞		5.85	5.69		5.67

5 97	8 29	868	14 13	7.65	9.6	% T	× 1.	301	6.16	6.19	6.22	4.74	4.74	5.65	5.68	11.74	11.74	2.95	6.22	76.9	14.68	7.36	7.04	8 77	5.1	5.01	5.01	4.17
20.6	6.75	5.31	11.86	13.56	7.84	4.85	4.85	3.02	27.56	6.93	5.89	8.04	8.04	5.79	4.11	7.05	7.05	2.06	6.27	7.26	8.27	6.23	6.65	662	4.75	6.71	6.71	1.52
11.47	7.87	5.84	14.66	14.88	6.93	9.7	9.7	4.52	69.9	6.73	5.96	5.46	5.46	5.88	5.84	20.74	20.74	2.41	6.62	11.57	9.61	5.45	99.9	6.64	6.83	4.02	4.02	3.53
7.66	6.93	3.59	11.49	20.85	96.9	5.85	5.85	2.81	12.83	7.18	4.61	8.29	8.29	13.64	4.85	34.17	34.17	1.95	2.49	7.57	8.03	7.65	11.74	4.79	6.18	5.16	5.16	2.97
8.57	6.81	8.11	13.07	9.85	8.9	7.39	7.39	3.24	7.51	5.1	7.46	4.61	4.61	5.52	5.97	16.97	16.97	2.89	5.01	8.18	7.35	6.42	7.38	2.92	4.67	4.13	4.13	1.87
5.61	9.87	3.76	10.64	10.33	10.85	5.67	2.67	2.62	8.07	8.7	4.16	5.14	5.14	6.17	3.84	5.4	5.4	. 2.19	3.65	8.18	5.51	6.56	9.12	5.59	4.2	4.71	4.71	2.61
6.61	4.76	14.34	2.91	2.64	6.68	10.13	10.13	5.46	3.46	3.71	7.67	6.22	6.22	8.99	7.87	0.76	0.76	9.24	8.74	2.96			3.56	5.79	5.01	8.14	8.14	5.4
6.84	9.57	6.51	4.68	4.4	6.17	3.65	3.65	10.11	5.78	6.24	5.98	5.22	5.22	3.81		1.4	1.4	5.62	5.49	3.49	3.93	5.06	5.21	7.55	6.74	4.39	4.39	7.18
5.17	5.35	4.05	3.98	6.35	6.21	3.96	3.96	6.48	5.1	4.81	6.48	4.88	4.88	5.21	8.52	1.18	1.18	5.94	6.02	4.53	2.61	3.94	3.16	5.7	6.91	5.86	5.86	8.13
5.01	14.43	6.03	5.55	3.88	6.31	5.45	5.45	9.97	3.19	4.92	5.94	5.25	5.25	3.84	5.18	1.06	1.06	6.4	5.27	6.4	2.52	7.41	7.15	5.12	3.95	6.04	6.04	7.34
8.04	7.88	16.71	3.33	2.88	8.02	16.76	16.76	6.56	3.61	4.19	9.13	6.45	6.45	11.03	10.23	0.78	0.78	13.23	9.71				5.71	10.88	6.78	8.78	8.78	6.45
8.42	12.01	. 14.85	3.05	3.99	5.91	10.62	10.62	5.84	2.58	3.75	: 8.07	69.9	6.69	10.46	7.93	0.83	0.83	10.63	9.87	89.			5.94	6.42	5.97	9.38	9.38	6.1

33/126

7.69		10.56	11.3		19.86	9.94	2.34	2.34	2.34	9.3	2.97	4.87	3.84	4.55	9.81	8.58	5.69	9	4.78	2.23	6.87	3.63	2.98	2.88	3.15	4.2	1.42	5.2	2.9
8.47	12.63	3.38	4.15	2.96	2.54	3.88	4.1	4.1	4.1	3.53	12.79	6.48	10.91	4.02	2.1	4.35	5.59	10.98	5.05	1.87	6.42	17.97	9.4	8.49	6.42	5.48	11.82	2.84	2.24
3.04	4.4	8.6	2.61	5.3	6.75	7.42	5.31	5.31	5.31	10.38	1:.	6.55	-	60.9	99.9	2.76	4.1	4.14	3.67	2.68	2.53	1.82	4.7	1.62	4.1	1.5	0.33	4.53	1.34
2.05	4.19	9.68	1.1	4.22	4.11	9	4.5	. 4.5	4.5	10.7	1.51	8.09	1.02	8.28	5.51	2.28	6.36	4.4	5.1	1.71	1.95	1.23	4.94	1.56	5.26	1.21	0.36	3.75	2.17
6.98	8.5	3.26	2.25	7	7.86	1.84	5.46	5.46	5.46	5.95	2.47	9.3	3.31	2.35	3.56-	8.35	3.15	7.45	5.84	0.89	3.43	3.2	2.44	6.43	8.15	[7]	1.52	3.43	4.06
5.8	9.31	5.23	3.29	4.85	2.21	4.73	6.03	6.03	6.03	2.64	99.9	5.23	5.84	6.23	2.38	4.12	4.76	5.35	5.45	3.98	3.86	8.6	4.08	5.37	5.35	5.79	5.12	4.39	3.74
10.13	8.86	5.19	5.69	3.92	2.42	5.27	6.19	6.19	6.19	2.53	6.38	4.44	5.38	6.58	2.54	4.7	6.57	7.9	4.86	3.54	7.66	6.92	3.83	4.78	5.27	8.3	4.45	4.97	2.87
								0.																					
SNI	AVPR18	PSMB8 v1	CDKN1C	CCL2	5.18 ALDH3A1	STIP1	LAIR1 WA	LAIR1 vB		NCOA2	<u>[</u>	ASCL 1	ITGA3 vB	85 85	PRKRIR	GF1	SLC6A7	GABRA2	XCR1	SLC11A2	SER.		IRF3	NR2F6	CSF3R v1	PCSK1N	PGDS	F144	HSPB1
5.59722222		5.413333333	5.38	5.222666667	5.18	5.03444444	5.028	5.028	5.028	4.96444444	4.931111111	4.868888889	4.796111111	4.69722222	4.65777778	4.59722222	4.59	4.55055556	4.540555556	4.49944444	4.488888889	4.485	4.461111111	4.373888889	4.266111111	4.173333333	3.97944444	3.97944444	3.92222222
5.597	5.471	5.413		2.222		5.034				4.964	4.931	4.868	4.796	4.697	4.657	4.597		4.550	4.540	4.499	4.488		4.461	4.373	4.266	4.173	3.979	3.979	2000

FIG.11-5A

3.86	0.17	2.54	7.79	5.2	1.88	3.15	2.53	2.53	2.53	2.52	5.31	2.98	5.52	2.27	4.14	3.06	2.98	1.96	3.76	7.88	3.52	1.9	3.72	4.38	3.49	5.3	5.08	3.53	5.19
2.91	0.5	2.68	5.89	6.92	1.67	2.91				2.12	5.94	2.96	4.81	3.3	5.67	3.4	2.35	1.18	4.95	7.18	4.27	3.33	4.53	4.13	2.79	4.55	4.43	7.66	90.9
6.26	0.00	2.14	8.13	99.5	2.7	2.59				2.17	4.24	3.68	4.8	2.23	3.68	3.52	3.77	1.42	4.79	7.44	4.03	1.87	5.61	4.89	2.43	3.06	4.31	3.32	5.81
5.57	0.39	2.45	3.68	4.49	2.24	2.76	. 1.31	1.31	1.31	1.89	5.14	2.96	-4.99	2.7	5.27	4.38	2.01	1.25	4.55	7.62	4.95	2.76	9.4.	5.14	2.79	3.39	6.88	2.43	90.9
6.3	0.16	5.16	5.75	5.4	1.99	3.23				2.77	6.62	2.58	5.58	3.71	5.45	3.34	3.56	1.19	3.29	9.13	6.36	2.53	2.57	3.71	5.42	-3.76	5.13	3.21	5.7
3.67	9.56	7.66	3.02	5.23	2.12	3.84	1.72	1.72	1.72	2	5.12	3.11	5.44	3.08	5.46	3.42	2.7	1.82	3.6	6.4	2.96	2.5	4.02	7.1	2.81	4.48	6.85	3.52	4.06
5.49		9.35	4.83		11.47	6.73	5.07	5.07	5.07	10.05	2.12	4.65	2.96	8.12	2.67	6.73	6.33	5.7	3.68	1.77	5.86	2.48	2.2	2.73	4.74	3.36	1.17	5.55	3
3.53	7.56	4.21	6.65	5.45	3.72	5.05	9.85	9.85	9.85	2.79	6.48	5.45	5.43	4.69	4.49	4.72	4.52	4.82	5.38	4.28	2.89	7.28	5.68	4.06	4.59	4.56	3.15	3.65	4.01
4.62	6.71	5.94	7.25	6.42	5.38	5.88	9.02	9.05	9.05	3.18	3.59	5.2	3.56	4.96	3.1	3.91	4.51	3.21	4.93	4.23	4.16	. 2.16	3.7	3.33	4.12	3.81	2.83	4.92	4.46
7.95	9.34	6.14	5.87	5.32	2.82	5.2	79.7	79.7	7.67	3.02	6.93	4.8	6.33	5.91	4.11	5.24	5.03	69.9	4.06	6.35	4.66	7.81	6.14	4.17	3.75	5.37	4.76	4.28	4.63
6.43	٠.	8.27	7.58		11.5	10.2	4.32	.4.32	4.32	11.82	3.38	4.31	4.95	5.48	4.24	5.89	8.64	. 6.45	3.99	1.81	4.42	2.74	2.16	3.96	2.16	5.3	. 2.02	. 5.45	2.3

FIG. 11-5B

35/126

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6.32	3.7	3.74	2.93	2.07	2.23	1.64	1.64	3.29	0.1	0.1	0.09	2.28	0.57	2.62	1.15	0.62	0.62	1.92	3.83		2.91	6.78		3.03	4.41	1.65	3.57	1.48	3.83
2.23	2.44	5.65	3.95	5.97	6.33	3.91	3.91	2.47	0.17	0.17		1.71	0.45	6.19	4.86	1.91	1.91	3.34	1.94	4.16	2.98	1.5	3.97	3.46	2.98	3.03	2.74	1.6	2.65
6.49	4.27	5.38	0.95	3.79	1.62	0.87	0.87	3.45			0.00	4.38	0.6	3.05	2.71	0.9	6.0	2.27	2.08	7.01	2.43	5.05	1.49	3.68	5.29	1.01	4.3	1.56	5.04
6.38	2.7	4.98	0.7	2.61	2.16	0.54	0.54	5.95	.0.02	0.02	0.05	4.3	0.63	3.29	2.96	-	-	4.45	1.51	4.54	1.32	4.68	1.74	2.38	5.04	1.24	4.2	1.74	4.17
5.29	7.49	8.26	2.23	5.28	4.84	0.8	0.8	6.07	0.08	0.08	0.11	4.75	1.03	5.43	2.47	2.27	. 2.27	3.34	2.16	3.37	3.92	3.15	3.46	2.12	4.14	4.15	4.01	2.88	3.63
2.3	3.05	3.51	2.55	4.72	3.3	2.98	2.98	2.8	0.09	0.09	0.1	1.54	0.43	4.19	5.63	1.72	1.72	2.85	3.48	3.82	7.86	1.22	5.35	3.81	2.49	3.01	3.06	1.39	2.08
2.72	2.97	3.57	3.96	5.55	3.69	5.72	5.72	2.33	0.08	0.08	0.08	1.22	0.38	3.27	4.43	1.86	1.86	2.64	3.67	4.88	3.18	1.89	4.92	6.34	2.84	2.02	3.42	0.72	2.15
		,																											,
CCR2 vB	TEX	LTA	DXT	HCRTR2	TNFSF9	PDCD4 v1	PDC04 v2	CYP2781	CMEB1 v1	GMEB1 v2	CHRM4	MMP3	HDC	NFKBIL2	IL-17RC	CISH v1	CISH v2	STAT1 vA	TGFA	ADRA2C	C074	IL3RA	MX1	Lest	INFRSF18	IRS1	AGTRL 2	POGFRB	NR4A2
3.910555556	3.88944444	3.855	35		3.58277778	3.575	3.575	3.501111111	3.489411765		(3.388333333	3.35444444	3.31.3333333	3.28888889		3.24444444				3.15277778	3.120714286	3.11944444	3.116666667	3.10777778	3.05944444	3.040555556	3.018333333
															Ĺ	Ĺ													

FIG.11-6A

SUBSTITUTE SHEET (RULE 26)

FIG.11-6B

3.04	4.88	2.61	6.64	2.72	3.5	9.91	9.91	3,35	. 10.62	10.62	6.12	3.19	3.95	2.63	3.09	5.99	5.99	2.67	4.06	0.34	4.83	2.05	1.47	2.71	2.14	4.08	1.6	6.69	2.21
2.11	5.46	1.96	4.59	2.5	3	5.8	5.8	4.08	7.78	7.78	10.54	9.31	10.74	2.43	2.96	8.15	8.15	6.52	3.69	0.46	5.62	2.47	1.79	2.12	2.27	4.25	1.82	6.9	1.94
2.79	4.45	3.78	6.47	3.17	4.72	3.85	3.85	4.58	11.46	11.46	6.95	4.28	5.33	2.16	2.36	4.12	4.12	3.69	3.08	0.31	3.21	2.7	2.24	1.67	2.56	4.92	2.18	3.96	2.99
3.63	4.85	2.62	5.52	2.35	3.93	2.12	2.12	2.94	8.43	8.43	14.02	8.73	16.56	3.36	2.44	9.19	9.19	4.69	2.83	0.49	3.96	3.28	2.01	1.3	2.22	5.23	1.62	6.58	3.8
3.41	4.23	2.4	4.84	2.87	3.34	7.54	7.54	3.54	11.92	11.92	9.94	3.59	7.81	2.49	2.29	6.07	6.07	5.55	4.42	0.39	3.71	2.5		2.65	2.52	4.57	2.08	6.14	2.02
3.26	5.07	2.87	5.78	2.15	2.08	4.29	4.29	3.2	8.23	8.23	10.37	2.95	10.11	2.62	2.1	4.26	4.26	3.25	3	3.86	4.48	3.24	1.99	1.87	2.91	4.37	2.05	7.05	3.7
5.42	3.03	4.37	2.72	3.37	2.37	1.49	1.49	3.28	0.05	0.05	0.05	2.57	0.45	3.23	2.33	2.82	2.82	2.21	3.11		2.42	5.78		3.64	3.48	1.91	5.01	1.13	2.55
2.18	3.27	4	2.7	5.09	3.74	3.63	3.63	3.13	0.07	0.07	0.07	1.75	0.5	2.53	5.37	1.74	1.74	2.5	2.71	4.05	1.79	1.7	3.54	3.7	3.14	2.72	2.03	0.98	3.25
3.85	2.72	2.97	2.58	3.24	3.7	2.54	2.54	3.45	0.09	0.09	60.0	1.77	0.56	3.11	5.53	2.02	2.02	1.96	3.6	4.74	2.71	1.51	3.21	4.02	2.26	3.11	2.65	1.45	2.96
2.34	2.29	3.01	3.05	4.66	3.52	4.67	4.67	2.45	90.0	90.0	90:0	1.14	0.37	3.64	4.39	1.43	1.43	2.7	4.14	4.99	1.41	1.68	6.51	3.7	2.03	1.47	2.48	1.11	2.26
6.63	3.14	3.71	3.27	2.89	. 3.42	2.05	. 2.05	2.66	. 0.07	0.07	0.08	2.13	. 0.52	4.14	2.57	3.13	3.13	1.85	3.67		3.13	5.57		3.95	.3.38	. 3.2	6.25	1.37	3.1

37/126

	Т						T		T	T				г	_	_		_									_		
1.6	3.29	1.59	2.33	0.2	3.87	3.41	3.41	0.79	3.12	-	4.62	3.15	1.92	1.92	3.46	1.67	2.38	1.8	5.56	1.89	4.73	2.68	4.14	4.14	1.35	1.7	1.7	1.7	1.7
1.99	0.48	2.88	1.63	0.05	8:	0.95	0.95	0.72	=	4.38	96.0	3.26	4.24	4.24	2.96	4.03	2.81	5.04	2.2	8.65	0.91	4.47	2.51	2.51	1.72	-4.04	4.04	4.04	4.04
1.36	0.58	3.33	1.73	90.0	1.62	1.41	1,41	0.46	1.28	4.71	0.96	3.53	3.56	3.56	2.77	4.31	3.57	3.35	2.35	11.18	0.71	5.08	2.96	2.96	1.28	3.86	3.86	3.86	3.86
2.48	1.83	2.3	3.81	0.08	3.34	2.02	2.02	1.03	2.41	3.19	1.85	2.67	2.91	2.91	2.81	1.79	4.82	3.58	2.01	1.99	0.95	5.17	4:32	4.32	0.91	0.99	0.99	0.99	0.99
0.94	3.77	2.92	3.43	0.12	3.81	3.26	3.26	1.12	2.71	1.13	5.87	3.83	2.03	2.03	2.57	3.5	2.78	2.53	2.82	1.27	2.82	1.58	2.96	2.96	1.5	2.45	2.45	2.45	2.45
1.66	2.48	2.39	1.76	0.1	3.5	3.48	3.48	1.07	4.21	1.21	4.48	4.09	1.99	1.99	1.87	3.73	3.01	1.91	2.23	1.55	4.88	1.55	2.86	2.86	1.56	2.51	2.51	2.51	2.51
IF127	SLC6A6	SLC6A8	EBI3	HTR1A	INSIG1	TRAF6 v1	TRAF6 v2	NOS3	PPP1R1B	INFSF6	PTCRA	FKBP8	DRD2 v1	DRD2 v2	SYN2 vIIb	sod1	BCL2 vB	NR.1	F0XA3	FKBP5	GSTA3	ALOX5AP	BLR1 v1	BLR1 v2	DRD4	TLR4 v1	TLR4 v2	TLR4 v3	TLR4 v4
2.965	2.95722222	2.930588235	2.864666667	2.85888889	2.83333333	2.831111111	2.831111111	2.78444444	2.781333333	2.776666667	2.771111111	2.74444444	2.735	2.735	2.724705882	2.70277778	2.696111111	2.68777778	2.687222222	2.681666667	2.67777778	2.671111111	2.62222222	2.62222222	2.588333333	2.57722222	2.57722222	2.57722222	2.57722222
	2	7	7	2	7	2	2	7	7	7	2.	2			2	2	2.	7	. 2.	2	2.	2.	2.	2.	2.	2.	7	2.	2

												3	8/	12	6														
4.34	4.5	4.56	1.72	4.31	1.05	2.31	. 2.31	8.56	3.13	2.96	3.26	0.48	2.32	2.32	1.6	0.64	2.37	0.81	2.85	0.77	3.38	1.89	2.08	2.08	4.18	2.86	2.86	2.86	2.86
2.09	4.49	2.98	2.7	7.26	1.05	2.65	2.65	4.82	2.86	2.73	2.28	0.5	2.95	2.95	4.05	0.82	1.93	1.25	6.68	0.71	2.05	2.09	2.01	2.01	6.44	1.92	1.92	1.92	1.92
3.71	3.52	3.74	4.83	5.97	1.39	3.3	3.3	8.16	3.46	3.73	3.23	0.43	2.12	2.12	1.96	0.65	1.65	1.23	2.22	0.53	1.58	2.42	2.04	2.04	6.54	1.8	1.8	1.8	1.8
2.25	5.88	3.22	3.74	15.16	1.94	3.31	3.31	2.61	3.16	3.51	3.2	0.48	3.56	3.56	4.22	0.56	1.2	1.64	1.61	0.36	1.18	1.89	1.93	1.93	5.69	1.31	1.31	1.31	1,31
1.99	3.63	3.67	2.47	7.58	1.51	5.35	5.35	6.59	2.95	4.03	3.35	0.51	2.73	2.73	1.58	1.01	2.33	0.66	2.83	0.75	2.85	2.4	2.99	2.99	. 3.4	2.7	2.7	2.7	2.7
2.85	5.17	3.2	3.06	10.15	1.13	5.04	5.04	6.24	2.98	3.69	2.55	99.0	1.3	1.3		0.53	1.83	1.48	1.7	0.65	2.36	2.04	2.01	2.01	2.46	2.6	2.6	2.6	2.6
5.11	3.21	1.67	3	0.04	5.7	1.8	1.8	1.51		3.51	1.35	4.58	3.46	3.46	2.48	3.45	3.63	4.17	1.71	6.36	3.19	2.66	2.45	2.45	0.7	3.66	3.66	3.66	3.66
2.14	1.42		3.65	0.09	1.96	3.53	3.53	0.9	2.83	0.85	3.02	3.5	3.58	3.58	3.11	3.33	2.81	2.67	2.72	1.24	3.1	2.5	2.97	2.97	2.43	1.96	1.96	1.96	1.96
2.89	1.87	3.19	2.99	0.08	2.26	7.67	79.7	0.9	2.21	1.24	2.51	3.55	3.04	3.04	1.96	4.78	2.64	2.44	2.61	1.52	1.69	1.99	2.74	2.74	2.41	2.35	2.35	2.35	2.35
3.07	1.57	3.65	3.12	0.09	4	3.37	3.37	1.18	3.3	1.21	3.57	3.07	2.29	2.29	2.11	4.94	2.71	2.12	7.66	1.49	4.71	1.79	1.93	. 1.93	1.87	2.08	2.08	2.08	2.08
5.8	3.32	2.13		0.06	6.52	1.41	1.41	2.36		3.69	1.24	5.27	2.38	2.38	3.83	3.6	3.27	4.69	1.37	4.09	3.2	2.62	1.9	1.9	0.99	4.41	4.41	4.41	4.41
7.1	2.25	2.4		0.02	4.55	1.69	1.69	Ţ.,	: .	3.21	1.58	5.85	2.85	2.85	. 2.98	5.31	2.79	7.01	2.24	3.27	3.91	. 3.26	2.4	2.4	1.16	3.19	3.19	3.19	3.19

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. 3.35	2.26	2.57	1.18	2.72	2.72	2.22	1.56	0.92	8.36	0.8	1.03	0.52	2.15	0.87	2.19	1.94	2.31	1.58	1.39	6.76	4.42	4.42	2.32	0.46	0.46	2.52	6.31	0.75	7.94
3.24	1.22	0.96	1.34	2.9	2.9	1.96	6.9	2.53	1.06	2.8	2.65	0.11	1.56	2.32	1.95	2.13	3.32	2.52	2.84	0.89	1.19	1.19	1.84	1.07	1.07	2.71	1.12	1.54	0.52
3.44	1.21	1.12	1.81	5.66	5.66	2.24	90.9	2.28	0.79	2.85	3.12	0.11	2.52	1.83	2.94	1.84	3.57	1.46	2.97	1.03	1.14	1.14	2.3	1.14	1.14	2.77	1.06	0.98	0.8
5.49	1.79	2.83	1.32	0.63	0.63	3.57	2.08	1.09	14	0.7	2.04	0.24		0.82	3.3	0.57	2.11	0.71	1.9	1	1.87	1.87	3.5	0.28	0.28	5.32	1.02	2.8	1.17
2.41	2.18	2.26	2.44	2.03	2.03	2.85	1.24	2.85	3.62	1.86	2.62	0.38	1.47	2.49	1.89	2.12	1.52	1.37	1.6	2.91	3.13	3.13	1.97	0.41	0.41	2.24	2.3	0.75	3.33
2.19	2.86	2.43	1.93	2.09	2.09	2.74	1.1	2.28	4.19	1.69	2.27	0.46	1.24	2.18	1.9	2.42	1.29	1.72	1.44	2.89	5.02	5.02	1.97	0.47	0.47	1.9	2.91	0.79	2.99
						*			•																111				
SPN	CALR	L17F	GREB1 va	PC v1	PC v2	TNFRSF21	NRIP1	APAF1 v2	FCERIA	HTR2C	CABRO	CALR3	ERBB2	MC4R	GPR51	RGS19IP1	ADMR	NR114	TLR10	SCAMP2	FKBP2 v1	FKBP2 v2	LCALS3BP	PDCFA v1	PDGFA v2	CCKBR	IRAK2	IPF1	TLR7
	2.53444444			2.48444444			2.45722222			5	2.38444444	Г	8		0	5	2.308333333	I	2.298888889	2.285	1	2.283888889	1	I		1	1	2.221111111	2.20444444
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1.93	1.93	3.95	3.48	2.46	2.46	2.8	99.0	2.73	1.16	2.54	2.22	8.49	2.97	2.25	3.21	3.05	1.74	5.04	1.96	2.12	1.29	1.29	2.36	6.26	6.26	1.84	1.96	1.49	1.76
1.89	2.78	2.31	2.86	2.5	2.5	2.19	1.69	2.38	1.51	2.45	2.63	5.78	5.24	1.93	2.18	3.26	2.72	3.11	1.89	2.28	1.26	1.26	2.36	4.31	4.31	1.53	1.88	1.38	1.57
2.84	1.74	4.76	2,36	1.73	1.73	2.4	0.76	1.8	1.55	2.74	2.77	8.5	3.43	3.57	2.74	3.31	2.43	3.5	2.52	2.55	1.35	1.35	7.66	4.31	4.31	2.62	7.06	1.96	1.51
2.09	5.09	2.63	4.06	1.56	1.56	2.26	2.05	2.12	1.86	2.96	2.43	3.83	3.32	4.03	2.36	5.09	4.02	3.43	2.47	2.29	2.12	2.12	3.44	6.58	6.58	1.31	79.7	2.82	1.64
1.82	2.92	2.25	4.22	2.84	2.84	3.59	1.25	3.86	1.56	3.53	3.9	7.33	3.13	3.44	2.02	3.44	1.98	4.73	1.93	2.06	2.32	2.32	2.2	6.71	6.71	1.48	2.12	1.77	2.29
2.33	2.31	2.13	2.05	1.36	1.36	2.13	0.63	2.03	1.4	3.02	1.79	3.14	2.74	3.82	2.63	2.21	3.54	3.89	2.25	1.98	2.14	2.14	2.74	0.48	0.48	1.34	1.79	2.21	1.38
2.57	3.69		1.43	2.12	2.12	1.86	4.77	1.9	1.33	2.06	1.54	0.34	1.92	1.5	2.44	1.66	1.35	1.38	3.41	0.8	2.63	2.63	1.57			2.73	0.94	3.4	1.05
2.22	2.07	2.87	2.38	2.45	2.45	2.96	1.34	2.7	3.61	2.17	3.1	0.7	1.9	1.96	2.46	2.15	2.35	1.26	1.95	2.94	1.61	1.61	2.22	0.52	0.52	2.24	3.13	0.29	2.72
2.07	2.51	2.18	4.19	6.78	6.78	3.16	1.74	3.84	1.73	2.18	3.31	1.48	1.6	3	2.17	2.1	1.84	1.31	1.6	2.53	2.18	2.18	2.01	0.51	0.51	1.91	1.6	0.41	2.72
1.65	5.66	2.57	3.17	4.22	4.22	2.56	1.66	4.15	4.27	2.21	2.84	0.71	1.48	1.65	1.86	2.72	1.84	1.79	1.41	4.07	2.5	2.5	1.84	0.51	0.51	1.78	3.87	0.8	3.58
2.49	3.5		2.08	1.47	1.47	1.47	3.99	2.27	1.27	3.04	1.19	0.34	1.31	1.34	1.72	1.76	1.52	1.63	4.96	0.9	2.35	2.35	1.82			2.06	1.87	9.48	1.09
S	5	_	V	2	2		2	2	2	1	1	7	2	9	4	6	-	_	6	3	6	6	5		_	-	2	9	2

FIG.11-8B

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1.98	7.99	2.34	2.22	1.94	0.75	2.69	1.67	4.95	1.42	2.28	2.28	2.03	1.1	1.42	1.31	1.07	2.87	1.03	1.89	4.03	0.49	2.7	0.22	17.1	1.38	1.7.1	2.17	1.21	2.05
0.74	0.34	2.72	2.73	4.38	2.37	2.27	2.21	- 88.	2.3	1.16	1.16	6.31	2.6	0.96	4.12	4.55	2.41	2.07	2.93	1.16	0.07	1.29	0.1	1.86	0.91	141	1.14	3.36	1.53
0.5	0.14	3.67	2.96	4.08	2.06	2.22	3.41	1.38	2.77	0.71	0.71	5.27	4.1	0.53	2.47	3.56	2.77	1.84	3.18	9.1	0.04	1.25	0.11	2.58	1.13	1.6	1.46	2.1	1.72
1.49	0.26	4.23	3.31	3.09	1.82	2.13	3.22	4.57	1.18	2.26	2.26	1.35	0.88	1.53	0.97	2.41	2.17	2.01	3.37	2.96	0.17	2.1	0.08	0.82	1.31	1.17	0.89	3.5	2.95
1.72	2.89	1.72	1.72	1.58	1.4	2.23	2.4	3.03	2.45	2.05	2.05	1.51	1.82	1.08	1.96	1.23	2.46	2.02	1.57	1.84	0.74	1.88	0.15	1.68	1.14	1.79	2.2	1.21	1.61
1.63	4.6	1.79	1.87	1.57	1.52	2.06	2.05	2.51	2.39	2.52	2.52	2.14	1.68	1.72	2.1	1.2	2.05	1.81	2.01	1.95	0.73	2.29	0.15	1.53	1.04	1.72	1.27	1.57	1.98
GRM6	IL12RB1	FCGR2A	GRAP2	TPO	CYP2B6	STAT2	INFRSF1A	SSI	ALDH9A1	CR1 vF	CR1 vS	980	RAG1	CHRM1	MASP2 v1	CIR	IFITW2	UCTREL1	CD84	CXCR3	NS	HSD17B8	WNT2	CHRNB2	CYP206	CX3CR1	IPT1	HRH2	GMEB2
2.19277778	2.187222222	2.178333333	2.154117647	2.138333333	2.12444444	2.120555556	2.103888889	2.087647059	2.083333333		_		2.03944444					1.94722222				_	1.907333333		1.88777778		1.844375	1.828235294	1.82444444 (

FIG.11-9A

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2.05	1.49	2.01	1.98	1.03	1.99	2.16	2.15	0.3	1.86	0.9	0.0	1.36	1.73	3.69	0.94	2.38	1.62	2.49	1.36	2.17	7.91	2.92	6.03	1.3	2.34	1.18	2.02	1.72	1.83
2.01	1.43	1.57	1.97	1.8	3.46	1.99	1.58	0.18	1.96	0.78	0.78	0.92	2.36	1.96	1.57	1.87	1.21	2.15	1.5	1.51	4.67	3.11	5.54	1.83	5.51	1.25		1.49	1.63
1.3	1.57	2.51	2.34	1.58	1.87	2.32	1.26	0.24	1.29	0.82	0.82	0.93	1.28	2.88	0.69	2.1	0.93	1.99	1.52	2.97	5.17	2.33	4.72	1.04	2.46	1.56	1.87	1.5	1.52
1.19	2.11	2.18	1.48	1.28	3.36	1.64	1.84		1.35	1.27	1.27	0.71	1.48	1.9	0.91	1.91	1.25	2.07	0.85	1.36	2.81	1.49	5.08	1.81	4.94	1.58		2.08	1.02
2.2	1.8	1.67	1.6	1.23	3.47	2.17	2.23	0.41	1.83	1.4	1.4	1.22	2.81	79.7	1.22	1.88	1.69	2.73	1.28	1.35	6.98	2.82	5.91	1.66	3.04	1.38	1.66	1.72	1.15
3.66	1.54	1.87		1.16	1.91	2.33	1.54	0.32	1.26	2.07	2.07	1.12	1.54	2.4	1.21	1.32	1.86	1.81	0.76	2.1	2.79	1.49	0.22	1.4	3.37	1.39	1.39	2.09	1.98
5.49	0.49	1.88	2.22	3.24	2.74	1.46	2.55	2.36	2.5	3.77	3.77	3.06	2.48	3.23	3.64		1.76	1.52	2.45	1,4	0.21	0.82		1.92	=:	2.71	3.07	2.61	1:69
1.16	4.09	1.92	2.24	2.15	1.53	2.59	2.14	2.55	1.81	1.48	1.48	1.43	1.58	0.83	1.75	1.47	2.28	2.27	1.92	2.11	0.55	1.56	0.1	3.94	0.99	2.34	1.48		1.87
1,53	2.67	1.82	1.93	1.86	2.35	2.23	1.84	2.98	2.19	1.6	1.6	1.56	2.15	1.04	1.97	1.63	3.04	2.35	1.59	1.54	0.49	2.39	0.1	4.27	1.29	1.66	1.25	1.61	1.64
1.47	4.82	1.57	1.64	1.34	4.1	2.5	1.84	1.84	2.57	1.72	1.72	0.31	2.15	1.04	2.12	1.49	2.55	1.96	1.9	1.89	0.61	2.09	0.1	2.36	1.01	1.93	0.89	0.54	2.49
5.74	0.77	 8.	2.12	2.3	2.48	1.6	2.16	2.86	3.02	4.27	4.27	2.84	1.9	4.59	3.7		1,41	1.55	2.44	1.41	0.14	0.92		1.38	9.0	3.14	4	0.76	2.3
3.61	0.37	1.94	2.29	2.88	.1.76	1.58	1.78	3.13	3,35	5.84	. 5.84	2.73	2.47	3.04	3.68		1.26	1.38	2.48	1.37	0.14	1.05		1.07	0.41	L	2.75	2.01	1.88

2.75	1.07	0.98	1.09	1.08	2.1	3.5	0.53	1.02	2.52	Ţ.	3.35	0.46	1.9	4.26	1.67	1.79	0.88	1.84	1.7	1.14	0.75	1.86	2.41	2.41	0.89	1.88	1.03	1.55	0.36
1.14	1.85	2.01	4.62	2.88	2.58	2.06	0.5	1.15	1.37	1.35	1.8	0.86	1.59	0.33	1.76	2.24	2.61	0.98	2.51	0.86	0.53	1.9	1.73	1.73	1.26	1.7	2.11	1.41	0.47
1.72	2.18	1.2	4.02	1.92	1.22	2.79	0.7	1.04	1.49	0.89	2.09	0.96	2.36	0.34	1.76	1.83	2.57	0.7	0.53	1.25	0.48	2.35	2.05	2.05	1.56	1.43	2.55	2.05	0.36
1.7	3.97	-	1.57	2.01	0.81	2.26	0.36	0.7	1.74	0.41	1.79	0.46	3.61		2.15	3.38	1.35	1.55	1.81	0.77	0.65	1.54	2.88	2.88	1.44	1.16	2.2	0.97	0.5
1.63	1.33	1.28	0.92	2.37	2.1	1.79	0.48	1.47	2.02	1.67	2.12	0.52	1.88	1.5	1.71	2.53	1.19	1.87	0.68	1.1	1.29	1.42	1.59	1.59	1.12	1.52	1.08	2.46	0.36
2.15	1.29	1.56	1.01	2.35	2.38	2.04	0.51	1.33	1.68	1.71	1.56	0.59	2.12	1.52	 8.	2.36	1.12	2.23	1.42	2.01	1.24	1.22	1.83	1.83	1.3	1.41	1.12	2.31	0.34
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PADIS	INFSF7	ARNTL	NGFRAP1	ALDH2	IBO	SLC6A9	TSE.	ADRA10	INSW1	53	JAK3	7 0032	NGFR	PTPN3	INSL3	CZWW	NTRK1	PLTP	So	ESR2	BDKRB2	\sim	1	,	1	1=	HM74	=	PER1
1.818888889 PA	1.81777778	1.81277778	1.80777778	1.79555556	1.786111111	1.770555556	1.751111111	1.75	1.73444444	1.730555556 F3	1.72944444	1.728666667	1.72388889 NO	1.71	1.696666667 IN	1.695625	1.68444444	1.658235294	1.64777778	1.642222222	1.636666667	1.620555556	1.608333333	1.608333333	1.605555556	1.603333333	1.591176471	1.583888889	1.56722222

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2.02	2.1	2.2	0.81	0.42	1.68	1.4	2.06	2.16	1.93	3.21	1.27	4.06	1.23	1.07	2	90.0	1.49	1.65	0.56	1.27	2.4	1.12	1.09	1.09	2.43	1.73	1.55	1.22	3.07
1.69	1.64	2.02	1.03	0.41	1.21	0.98	4.39	2.33	2.23	2.3	1.35	2.88	98.0	5.38	1.69	0.09	1.86	1.34	0.45	2.15	2.02	1.83	0.94	0.94	2.92	1.39	1.57	0.89	1.13
2.16	1.83	1.9.	0.97	0.34	2.71	1.12	3.32	2.17	1.75	2.89	1.9	4.47	98.0	1.6	2.16		1.55	1.47	0.56	2.29	2.45	1.62	1.16	1.16	2.21	1.9	1.92	1.09	7.22
2.79	1.4	2.4	1.09	0.37	1.06	0.58	6.45	3.98	2.21	1.76	1.49	4.19	1.15	3.61	1.43	0.14	1.86	1.33	0.44	1.58	2.57	3.17	0.62	0.62	1.61	1.74	1.95	1.29	6.18
1.65	2.11	2.22	1.17	0.44	1.76	1.09	5.21	2.28	1.56	5.69	1.32	4.58	96.0	1.6.1	1.48	0.09	1.5	1.53	0.63	2.25	2.97	1.36	0.71	0.71	2.37	1.75	1.65	0.73	4.5
2.8	2.03	3.21	1.19	0.51	1.29	1.01	4.22	2.38	1.98	1.35	2.51	0.55	1.59	1.79	2.12		1.21		0.54	1.7	1.7	1.63	1.54	1.54	2.81	1.82	1.1	1.01	1.29
1.4	1.73	1.75	3.71	2.59	1.83	1.62	0.5	0.52	1.43	0.0	1.05		2.12	0.48	1.09	1.51	2.43	1.82	4.46	1.94	0.85	0.92	1.88	1 .88	1.49	1.44	1:1	1.35	0.41
1.67	1.56	1.5	1.63	2.45	1.23	3.01	0.37	2.57	0.96	1.76	2.07	0.5	1.85	1.47	1.89	2.94	0.89	1.74	1.35	2.3	1.5	1.92	1.72	1.72	1.18	1.34	1.67	2.11	0.39
1.38	1.86	1.79	1.26	2.92	2.82	1.32	0.39	2.16	1.58	2.04	1.43	0.45	1.69	1.02	1.73	2.17	1.16	2.31	1.58	2.89	3.51	1.41	1.08	1.08	1.13	1.23	1.67	1.71	0.39
1.62	1.86	1.58	1.16	2.44	1.68	2.54	0.69	2.04	1.33	7.67	1.92	0.4	1.51	1.72	1.85	- 2.67	1.13	1.87	1.71	1.93	1.93	1.34	1.83	1.83	1.1	1.58	1.34	1.82	0.34
1.27	1.49	1.59	2.11	3.27	2.08	1.24	0.42	0.99	2.18	1.11	1.16		1.98	0.67	1.32	1.8	2.52	2.06	4.69	1.19	0.81	1.25	2.11	7.11	1.15	1.96		2.22	0.51
1.2	1.42	2.43	3.18	3.55	1.61	1.52	0.42	1.21	1.26	1.34	0.95		1.77	0.7	0.93	1.53	3	1.9	4.04	0.94	1.81	1.31	1:78	1.78	0.93	1.88	1.43	2.32	0.39

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1.58	1.78	0.49	0.98	0.98	1.58	1.14	1.36	.68	2.26	0.77	1.18	2.53	0.98	1.64	1.31	1.62	2.92	0.83	1.37	0.91	2.72	1.26	0.93	0.6	0.67	1.19	1.29	1.57	0.0
2.65	1.98	2.36	1.78	1.78	1.44	1.3	0.91	1.12	0.92	0.49	1.27	96.0	1.75	1.07	1.37	1.53	1.75	1.78	0.42	0.99	0.5	0.9	9.0	3.41	1.2	3.22	1.86	1.38	2.87
1.05	2.3	1.16	1.79	1.79	1.94	1.89	1.85	2.07	2.48	0.56	0.69	1.34	1.61	5.06	1.68	1.88	0.75	1.53	0.98	1.4	2.24	2.02	0.92	0.91	0.74	0.32	0.81	3.76	0.55
1.49	2.54	1.05	1.97	1.97	1.98	1.76	2.32	2.23	2.24	0.5	1.03	0.71	1.62	2.07	1.95	2.18	0.67	1.49	1.04	1.53	3.25	2.49		0.89	1.13	1.12	0.98	3.17	0.47
3.73	2.45	1.15	2.05	2.05	1.85	2.55	0.73	5.13	96.0	0.4	2.05	1.1	1.9	5.66	2.63	2.78	1.48	1.34	0.58	2.85	1.25	1.99	2.06	1.18	1.99	2	0.99	1.26	0.94
2.41	2.43	2.12	1.43	1.43	1.63	1.46	1.23	1.57	1.15	1.54	1.57	1.14	1.96	1.08	1.44	1.23	1.21	1.85	1.62	1.06	0.98	0.68	1.29	3.4	1.36	2.37	1.44	0.71	2.08
2.69	2.28	1.32	1.32	1.32	1.01	1.33	1.52	1.69	1.28	1.03	1.29	1.29	1.33	1.15	1.27	1.18	2.43	1.44	1.28	0.97	0.81	0.79	0.76	3.23	1.07	3.35	1.88	0.74	1.51
PTPRN	OR05	L12RB2.	TRIM34 v1	TRIM34 v2	CYB561	CYP11A	DLG3	CYP4B1	CCR1	CHRNA5	HLA-DPB1	BCL2 vA	TIMP2	IL4R	CHRNE	PRDM2 v1	PRSS11	CIAS1	PTGFR	CRYAB	MAP2K4	СКНВР	ADCYAP1R1	SPC	PTGER1	NR1H2	CHRM3	ENO1	CSF2
1.56444444	1.552352941	1.546666667	1.544117647	1.544117647		1.52444444	1.521111111		1.495555556	1.493333333			1.481764706	1.478333333		1.466111111		1.453333333	_	_	1.441111111	1.433333333	1.430625	1.426666667	1.42222222	1.407647059	1.395555556	1.39277778	1.368333333

FIG.11-11A

0.91	0.07	1.79	1.37	1.37	1.33	1.7.1	1.94	0.51	1.7.1	2.87	2.49	2.04	1.18	1.44	1.28	96.0	1.28	1.44	1.47	1.05	0.97	1.76	2.25	0.95	2.08	0.09	2.26	0.89	1.87
1.25	0.12	1.56	1.21	1.21	1.67	1.03	2.37		1.14	2.22	1.72	1.77		1.17	1.18	2.04	1.03	1.55	2	3.62	0.78	1.43	1.45	1.12	1.68	0.07	1.23	1.16	1.62
0.8	0.09	. 1.08	1.81	1.81	1.75	2.18	1.22	0.46	1.31	1.78	1.6	1.25	1.37	2.17	1.68	0.96	1.66	1.3	2.37	0.98	0.95	2.31	1.61	96.0	2.83	0.16	1.61	=	1.98
0.58		2.14	1.49	1.49	2.18	1.64	1.41	0.43	0.98	2.52	1.96	1.26	1.38	1.7	1.49	0.77	1.52	1.71	1.63	1.09	0.88	. 2.12	7.66	0.9	2.29	0.18	1.43	1.27	. 1.33
0.83	0.11	1.44	1.52	1.52	0.88	1.63	2.29	0.34	1.3	3.67	1.84	1.95	1.77	1.26	1.13	0.36	1.46	1.3	2.59	1.03	1.34	1.47	2.35	1.14	1.74	0.07	1.78	1.39	1.6
0.61	0.14	1.21	2.47	2.47	0.97	1.39	1.78	0.39	1.19	1.51	1.79	0.77	1.58	1.24	1.75	0.7	0.93	1.27	2.08	2.93	0.96	1.91	1.35	0.9	1.69		1.34	0.9	2.23
1.35	1.67	0.75	1.1	1.1	1.03	1.03	1.46	1.51	1.94	0.5	1.37	1.55	99.0	1.33	1.27	1.89	1.66	1	0.89	1.32	1.97	1.04	1.02	0.72	0.74	1.69	1.35	2	0.43
1.78	2.45	2.64	•		1.9	1.45	0.85	1.76	1.19	1.34	1.06	- 1.24	1.59	1.18	1.35	1.39	0.81	1.53	1.41	. 1.04	1.24	0.99		1.4	1.28	2.31	1.29	0.69	1.42
1.34	2.49	2.87	1.27	1.27	1.82	1.4	1.19	1.93	1.67	2.35	1.41	1.66	2.23	1.32	1.23	1.21	0.78	2.04	1.66	1.23	1.79	0.85	1.68	1.96	1.18	1.45	1.23	0.95	0.94
1.74	1.67	2.13	1.45	1.45	1.6	1.28	1.32	1.57	1.2	2.21	1.31	1.4	1.37	0.88	1.04	1.08	1.54	1.77	1.48	0.98	1.82	0.4	1.18	1.6	1.14	2.24	0.77	0.72	1.64
1.37	1.82	0.58	.1.24	1.24	1.23	1.27	1.63	1.21	. 2	. 0.62	1.21	2.88	. 0.91	1.19	1.34	2.03	2.43	0.99	1.09	0.97	1.49	1.39	0.78	0.41	0.79	2.1	1.58	1.41	0.55

FIG.11-11B

47/126

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0.75	1.69	0.99	1.37	0.62	0.62	0.74	2.02	0.22	1.1	0.56	0.56	0.56	0.56	0.56	1.06	1.06	1.06	1.06	1.6	0.22	. 1.73	1.73	1.76	0.74	0.7	0.7	0.7	1.3	1.39
1.2	2.62	2.3	0.92	2.28	2.28	0.51	4.35	0.25	0.65	2.17	2.17	2.17	2.17	2.17	3.13	3.13	3.13	3.13	1.32	0.22	1.25	1.25	1.65	1.26	0.58	0.58	0.58	1.44	1.7
1.94		1.29	1.29	1.11	1.11	0.68	1.15	90.0	1.45	0.48	0.48	0.48	0.48	0.48	0.29	0.29	0.29	0.29	1.54	19.27	. 2.17	2.17	2.16	1.07	0.77	0.77	0.77	1.95	0.75
1.21	0.34	1.16	1.23	1.12	1.12	0.82	0.65	0.06	1.47	0.53	0.53	0.53	0.53	0.53	0.46	0.46	0.46	0.46	2.01	0.21	1.26	1.26	1.65	0.8	0.86	0.86	98.0	1.45	0.99
2.08	0.91	2.51	1.26	0.88	0.88	1.05	2.98	0.11	1.18	1.04	1.04	1.04	1.04	1.04	1.82	1.82	1.82	1.82	1.19	0.2	0.79	0.79	1.92	0.75	1.25	1.25	1.25	1.43	1.7
1.47	1.66	1.55	0.97	1.36	1.36	0.4	1.62	0.25	0.79	1.19	1.19	1.19	1.19	1.19	1.93	1.93	1.93	1.93	1.31	0.12	1.13	1.13	96.0	1.39	0.89	0.89	0.89	1.31	1.29
5.7	3.79	1.17	. 1.05	1.36	1.36	0.37	2	0.28	0.83	1.08	1.08	1.08	1.08	1.08	2.2	2.2	2.2	2.2	1.47	0.11	1.65	1.65	1.02	1.48	0.7	0.7	0.7	1.08	1.67
1.36 APCS		1.348333333 MKNK2	1.342941176 TBXAS1 vTXS-I	1.341666667 SNAP23 v1	1.341666667 SNAP23 v2	1.32944444 CCL18	1.325294118 TAF9 v1	1.31944444 CYP1A1	1.31944444 GRIN2D	1.313888889 DRD3 vA	1.313888889 DRD3 vB	1.313888889 DRD3 vC		1.313888889 DRD3 vE	1.306111111 NRG2 v1	1.306111111 NRG2 v2	1.306111111 NRG2 v3	1.306111111 NRG2 v4		1.296470588 IFI16	1.29444444 CXCL5	1.29444444 CXCL6	1.292 <i>777778</i> CNOT2		1.27833333 SYN3 villa		1.278333333 SYN3 vIIIc	1.275 CST3	1.271666667 TRPV2

FIG.11-12A

FIG. 11-12B

1.41	0.49	1.07	1.68	1.81	1.81	2.32	0.23	4.34	1.82	1.6	1.6	1.6	1.6	1.6	0.9	0.9	0.9	0.9	0.49	0.15	1.12	1.12	-	2.17	1.96	1.96	1.96	0.87	0.97
11:1	0.4	1.52	1.06	1.86	1.86	3.34	0.19	4.47	2.39	1.39	1.39	1.39	1.39	1.39	0.75	0.75	0.75	0.75	0.54	0.09	1.39	1.39	1.59	1.85	2.07	2.07	2.07	1.6	1.5
1.5	0.71	0.8	1.47	1.7	1.7	2.77	0.2	3.85	1.53	2.24	2.24	2.24	2.24	2.24	0.8	0.8	0.8	0.8	0.48	0.22	0.9	6.0	1.31	1.76	2.06	2.06	5.06	1.29	0.86
0.92	0.95	1.22	1.56	1.45	1.45	3.74	0.19	2.22	1.67	1.74	1.74	1.74	1.74	1.74	111	1:1	1.1	1.11	0.59		1.1	1:1	1.18	1.12	3.16	3.16	3.16	0.95	0.76
1.3	0.67	1.09	0.93	1.88	1.88	1.85	0.19	4.12	1.76	1.71	1.71	1.71	1.71	1.71	1.01	1.01	1.01	1.01	1.09	0.25	1.1	1.1	1.02	1.39	1.85	1.85	1.85	1.18	1.79
1.24	0.55	1.09	1.18	1.9	1.9	3.16	0.38	2.52	1.86	2.89	2.89	2.89	2.89	2.89	1.5	1.5	1.5	1.5	0.76	0.15	1.18	1.18	0.95	1.51	2.41	2.41	2.41	0.74	1.36
1.39	1.95	1.15	1.97	0.95	0.95	0.64	1.34	0.18	1.14	0.53	0.53	0.53	0.53	0.53	1.3	1.3	1.3	1.3	2.98	0.24	1.93	1.93	1.03	1.21	0.58	0.58	0.58	1.23	0.53
1.34	1.36	1.53		0.91	0.91	0.32		0.19	1.02	1.47	1.47	1.47	1.47	1.47	1.52	1.52	1.52	1.52	1.27	0.13	1.02	1.02	1.27	1.21	0.45	0.45	0.45	1.69	1.43
1.5	0.84	1.37	2.07	0.6	9.0	0.4	1.71	0.5	1.03	0.99	0.99	0.99	0.99	0.99	1.03	1.03	1.03	1.03	1.44	0.15	0.89	0.89	0.91	1.14	0.0	0.0	0.0	1.27	1.97
1.47	1.56	1.18	1.21	1.59	1.59	0.37	1.27	0.27	1.21	1.39	1.39	1.39	1.39	1.39	1.64	1.64	1.64	1.64	1.25	0.07	1.19	1.19	0.81	0.86	1.08	1.08	1.08	1.14	1.47
1.15	2.55	1.28	1.61	. 0.77	0.77	0.45	3.06	0.16	. 0.85	0.65	0.65	0.65	0.65	0.65	1.06	1.06	1.06	1.06	2.14	0.24	1.5	1.5	1.08	1.42	0.74	0.74	0.74	1.03	0.76

49/126

FIG. 11-13B

0.34	1.34	1.08	1.46	1.21	1.21	 89.	1.14	0.99	1.33	1.04	2.09	1.23	1.3	1.3	1.3	1.01	1.55	0.73	1.24	1.24	1.05	1.05	1.04	1.37	0.62	0.66	1.8	0.33	2.19
0.44	1.44	0.73	5.05	1.57	1.77	2.19	1.32	0.86	0.82	0.7	1.65	1.03	1.56	1.56	1.56	1.49	1.27	0.64	0.88	0.88	1.19	1.19	1.05	0.69	0.54	0.5	1.3	0.55	1.43
0.48	1.27	1.33	1.23		0.98	3.87	1.64	1.18	1.32	0.94	1.56	1.29	1.25	1.25	1.25	1.48	1.59	0.76	0.97	0.97	0.86	0.86	0.95	0.56	0.65	0.56	1.4	0.41	1.61
0.43	0.66	1.34	1.43	1.05	1.05	1.16	1.36	1.07	1.12	9.0	1.91	1.2	1.83	1.83	1.83	6.33	0.0	1.05	0.79	0.79	0.85	0.85	0.59	0.78	0.61	0.56	1.22	0.37	2.09
0.37	1.56	1.34	1.46	1.2	1.22	1.3	1.32	0.84	1.07	0.81	1.57	0.99	1.37	1.37	1.37	1.45	1.24	0.54	0.88	0.88	1.49	1.49	0.89	1.02	0.63	0.91	1.38	0.86	
0.3	1	2.45	1.7	1.01	1.39	1.05	1.23	1.21	1.85	0.93	1.6	1.47	1.41	1.41	1.41	3.38	1.31	0.63	1.05	1.05	0.98	0.98	0.81	1.08	0.39	0.7	1.29	0.57	-
3.33	0.76	0.71	0.69	1.79	1.7	0.58	1.4	0.43	0.93	0.97	0.68	0.65	1.07	1.07	1.07	9.0	0.92	1.38	0.8	0.8	0.68	0.68	0.78	1.79	1.42	1.71	0.97	1.01	
0.74	1.31	1.07	1.09	0.7	0.98	1.11	1.3		1.16	1.36	0.9	1.46	1.09	1.09	1.09	. 0.37	1.12	0.99	1.03	1.03	1.48	1.48	1.91	1.02	1.48	1.01	1.02	1.03	0.81
0.64	1.91	0.73	1.09	0.97	0.0	1.03	1.2	1.19	0.93	0.85	1.06	0.65	1.13	1.13	1.13	0.49	0.39	-	1.14	1.14	1.17	1.17	0.87	1.34	1.38	0.97	0.86	1.7	0.55
99.0	1.47	1.38	96.0	0.73	1.04	0.92	0.83	2.92	1.08	1.58	1.01	1.74	0.91	0.91	0.91	0.32	0.84	0.83	2.64	7.64	1.77	1.77	1.57	1.9	1.23	1.4	1.32	1.28	1.36
4.13	0.65	0.71	. 0.55	1.69	2.29	0.56	0.92	0.47	1.24	1.12	1.19	1.2	1.23	1.23	1.23	0.53	0.83	.1.48	1.16	1.16	0.55	.0.55	1.59	1.28	1.3	2.17	0.0	. 1.83	

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0.43	0.59	1.41	0.47	1.04	1.85	1.78	1.15	0.25	1.08	1.44	1.6		0.51	0.75	0.75	0.75	1.36	0.86	1.26	0.34	0.54	1.83	0.41	0.88	1.03	1.49	0.61	0.92	0.77
0.38	3.1	1.02	1.35	0.76	1.05	0.73	1.09	0.27	1.23	0.55	1.69	1.27	0.32	1.07	1.07	1.07	0.98	0.75	1.17	0.41	1.07	1.52	0.91	0.92	1.53	0.52	1.18	1.53	1.13
0.58	0.19	0.87	0.32	1.58	0.99	2.24	0.97	0.23	1.54	1.61	0.46	0.43	0.15	1.61	1.61	1.61	2.47	0.99	99.0	0.31	-	1.21	0.6	2.01	1.06	1.22	96.0	1.3	1.44
0.37	0.28	0.77	0.57	1.07	0.9	2.59	1.13	0.18	1.29	1.52	.0.3	0.73	0.14	1.31	.1.31	1.31	2.72	0.89	0.34	0.27	0.81	1.54	0.45	3.51	1.13	1.89	0.75	1.26	1.5
1.33	0.52	1.06	1.19	0.61	0.83	99.0	1.3	0.35	0.53	0.68	0.25	1.1	0.48	0.7	0.7	0.7	0.79	1.73	0.61	0.34	2.12	1.48	0.56	0.42	1.27	1.83	2.08	1.37	1.12
0.79	1.77	1.52	1.3	1.2	1.19	0.83	1.03	0.51	1.23	0.48	1.33	1.01	0.49	1.09	1.09	1.09	0.67	1.08	0.84	0.55	1.07	1.14	1.03	0.72	0.87	0.52	1.05	0.82	0.61
0.64	1.64	1.6	0.73	1.43	1.08	0.92	0.73	0.44	1.65	0.56	2.08	1.45	0.44	1.22	1.22	1.22	0.91	1.03	1.46	0.54	0.94	1.45	1.01	0.89	0.73	0.49	0.94	0.85	0.67
							-	•				•																	
CD34	CCR5	RAMP1	FCGBP	1.1 CD38	IF135	SLC18A2	ACE v1	SLC25A4	(ANXA8	L19	CRB7	CD3D	GALR2	CASP4 va	CASP4 vc	CASP4 vd	TRIP	C10B	TIMP3	1LR2	CSF3	PIGR	IL 15RA	POLE4	ALDH1B1	TANK v1	CLOCK	THPO	MADD v1
		.105555556	1.103333333	1.1		.083888889	.07277778 ACE v1	1.07055556	.038333333		1.026470588	1.025	.021111111	.018333333		.018333333	87.7777710.1	.015555556	1.01111111		1.000555556		0.993333333		0.98722222		_	0.955	0.953333333
		1	-			1	-	1,	-		1		•		,	1					-	0	0	0	0	0	0		0

FIG.11-14B

2.57	1.14	0.99	0.67	-	0.89	0.52	0.78	3.67	0.76	1.1	0.99	1.03	2.84	0.94	0.94	0.94	0.29	0.95	0.99	2.34	0.72	0.07	1.63	0.56	0.65	0.62	0.78	0.86	1.09
2.09	0.96	0.71	1.12	1.04	0.97	0.67	9.0	1.45	0.72	0.94	0.67	1.26	1.97	0.79	0.79	0.79	0.34	1.41	0.74	1.15	0.74	0.03	1.97	0.55	0.63	1.03	0.79	0.65	1.14
2.2	0.85	0.68	0.78	0.75	1.03	0.46	1.11	2.68	0.68	1.33	0.71	1.29	2.02	1.12	1.12	1.12	0.42	0.98	0.63	4.57	1.48	0.08	1.64	0.62	1:21	1.11	1.06	0.68	0.89
1.77	1.06	0.72	3.74	0.0	1.29	0.57	1.21	2.08	0.49	1.45	0.48	1.02	1.59	0.84	0.84	0.84	0.29	0.81	0.9	0.94	1.08	0.13	1.24	0.37	1.33	0.91	0.83	0.44	0.85
2.15	0.96	1	1.76	1.04	0.93	0.71	0.96	3.14	0.92	1.34	0.8	0.83	1.98	0.93	0.93	0.93	0.48	0.88	0.75	1.62	0.79	0.18	1.57	0.71	0.57	0.67	0.76	0.59	1.02
1.92	1.3	0.84	3.03	1.27	1.18	0.67	0.68	2.26	0.61	1.03	0.99		2.91	1.01	1.01	1.01	0.72	0.0	0.64	1.2	1.12	0.11	1.38	0.52	0.6	0.57	0.98	0.55	1.07
0.34	0.56	1.04	0.5	1.35	1.11	1.86	0.81	0.22	1.36	1.6	0.95		0.46	1.34	1.34	1.34	1.91	0.88	1.01	0.72	0.84	1.45	0.55	1.54	0.88	1.28	0.82	1.1	0.85
0.61	1.41	1.62	0.66	0.94	0.9	0.87	1.42	0.38	0.77	0.54	1.64	1.06	0.43	1.04	1.04	1.04	· 0.83	1.33	1.36	0.52	1.09		0.9	0.68	1.02	1.02	1.11	1.31	0.89
0.53	0.36	1.69	0.75	1.17	0.36	1.03	2.35	0.45	0.83	0.57	1.21	0.94	0.53	0.88	0.88	0.88	0.76	0.88	0.36	0.93	0.95	0.81	0.67	0.78	1.51	0.83	1.05	1.08	0.74
0.94	1.88	1.43	0.48	1.35	0.88	0.75		0.5	1.48	0.52		0.93	0.44	0.88	0.88	0.88	0.81	1.07	1.92	0.62	0.86	1.61	0.89	0.75	0.72	0.64	0.82	96.0	0.83
0.38	0.76	0.93	0.44	1.3	1.58	. 1.65	0.99	0.21	1.52	1.4	1.3		. 0.68	0.81	0.81	0.81	1.57	0.86	1.96	0.81	0.79	2.28	0.47	1.38	1.03	1.04	0.76	0.92	0.55

53/126

																	-												
0.77	0.77	0.77	0.77	0.77	0.77	0.77	-	2.12	0.9	0.91	0.42	0.56	1.41	1.41	1.41	1.41	0.65	0.54	0.46	0.51	1.34	1.68	0.3	0.15	1.65	0.38	0.71	0.93	0.71
1.13	1.13	1.13	1.13	1.13	1.13	1.13	1.14	0.54	1.84	0.76	0.76	0.81	0.92	0.92	0.92	0.92	1.26	1.04	1.21	1.35	0.55	0.52	0.51	0.21	0.37	96.0	2.67	0.81	0.54
1.44	1.44	1.44	1.44	1.44	1.44	1.44	0.97	1.07	0.82	0.65	0.57	0.84	1.02	1.02	1.02	1.02	0.36	0.57	0.72	0.53	0.79	0.83	0.5	0.12	2.47	0.31	0.24	0.85	0.73
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.33	0.69	0.88	0.76	0.58	0.79	1.02	1.02	1.02	1.02	0.56	0.69	0.7	0.55	0.72	0.93	0.27	0.11	2.1	0.33	0.24	1.2	1.51
1.12	1.12	1.12	1.12	1.12	1.12	1.12	1.38	1.17	0.78	1.2	0.61	0.44	0.93	0.93	0.93	0.93	0.55		0.91	0.99	0.81	0.94	0.4	0.22	1.1	0.79	0.31	1.69	1.19
0.61	0.61	0.61	0.61	0.61	0.61	0.61	0.78	0.43	1.1	1.15	0.84	0.86	8.0	8.0	0.8	0.8	0.8		0.73	1.03	0.89	0.97	0.92	0.15	0.36	0.9	1.32	0.91	0.76
0.67	19:0	0.67	29.0	0.67	79.0	19.0	0.73	0.46	0.95	0.9	0.84	0.73	1.05	1.05	1.05	1.05	0.48	0.92	0.71	1.14	0.88	1.16	0.63	0.14	0.36	0.86	1.31	0.0	0.67
) v2) v3) v4	. 15	9 v (/A (8 v	94	<u> </u>	1781	JA13		·							10 vB	363	F5	71		-DRA	=	A1	HS017B3	01	1 vGAD25
0.95333333 MADD v2	0.95333333 MADD v3	0.95333333 MADD v4	0.95333333 MADD v5	0.95333333 MADO v6	0.95333333 MADD v7	0.95333333 MADD v8	0.94555556 CYP46	0.943333333 FCGRI	0.93 HSD178	0.92777778 SLC6A13	0.92055556 LST1	0.91944444 WASF	0.918125 ADA	0.918125 ADA	0.918125 ADA	0.918125 ADA	0.91222222 ELK1	0.905294118 NOS	0.89333333 CASP10	0.889411765 GABRG3	0.886666667 TNFSF5	0.886666667 CCL21	0.88222222 NR2F	0.88 HLA-DRA	0.876666667 LTA4H	0.87444444 NR5A1	0.871176471 HSD	0.87 CDF10	0.863333333 GAD1 vGAD25

FIG.11-15A

1.09	1.09	1.09	1.09	1.09	1.09	1.09	0.78	0.65	0.72	0.98	1.28	1.24	0.37	0.37	0.37	0.37	1.03	1.04	1.36	1.25.	0.57	0.53	1.33	1.11	0.57	0.91	0.45	0.56	1.13
1.14	1.14	1.14	1.14	1.14	1.14	1.14	0.61	1.04	0.84	1.33	1.2	0.91					0.83	1.02	1.26	0.94	1.14	0.58	1.54	1.09	0.45	0.57	0.54	0.52	1.11
0.89	0.89	0.89	0.89	0.89	0.89	0.89	0.81	0.62	1.03	0.85	0.79	1.13	0.41	0.41	0.41	0.41	1.41	1.36	0.98	0.92	0.84	0.52	1.44	3.46	0.55	1.98	0.48	0.77	0.89
0.85	. 0.85	0.85	0.85	0.85	.0.85	0.85	0.64	0.98	1.07	0.94	1.01	1.02	0.71	. 0.71	0.71	0.71	1.37	0.74	1.54	1.06	0.73	0.53	1.57	3.36	0.5	2.55		0.55	0.86
1.02	1.02	1.02	1.02	1.02	1.02	1.02	0.76	0.82	0.75	0.96	1.06	1.14	0.82	0.82	0.82	0.82	1.29	0.92	0.97	0.88	0.95	0.58	1.7	3.41	0.61	1.98	0.51	0.61	1.24
1.07	1.07	1.07	1.07	1.07	1.07	1.07	9.0	0.89	0.69	1:1	1.15	0.78					1.08	1.4	1.07	0.89	0.81	0.54	1.16		0.48	0.53	0.69	0.67	0.76
0.85	0.85	0.85	0.85	0.85	0.85	0.85	1.48	2.03	0.55	0.83	1.17	· 0.4	1.26	1.26	1.26	1.26	0.31	9.0	9.0	0.61	0.91	1.98	0.25	0.7	1.59	0.37	0.79	0.77	0.78
0.89	0.89	0.89	0.89	0.89	0.89	0.89	1.14	0.49	1.49	0.91	1.03	1.03	0.86	98.0	0.86	0.86	0.78	1.15	0.58	99.0	0.93	0.75	1.05	0.15	0.31	0.89	1.29	1.1	0.65
0.74	0.74	0.74	0.74	0.74	0.74	0.74	1.04	99.0	0.89	1:1	1.28	2.03	0.81	0.81	0.81	0.81	2.42	1.02	0.94	0.93	1.32	0.73	1.14	0.16	. 0.45	0.53	0.71	0.93	0.69
0.83	0.83	0.83	0.83	0.83	0.83	0.83	0.77	0.49	0.82	0.74	1.03	1.35	0.76	0.76	0.76	0.76	0.66	0.36	0.59	0.88	0.93	0.66	0.81	0.09	0.36	0.62	1.75	0.9	0.74
0.55	0.55	0.55	0.55	0.55	0.55	0.55	1.06	1.83	0.61	0.63	0.95	0.49	1.54	1.54	1.54	1.54	0.52	0.42	0.75		. 0.85	. 1.53	0.36	0.17	1.5	0.28	0.8	66.0	0.58

FIG.11-15B

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0.71	1.07	1.46	0.57	1.12	1.12	1.12	1.12	1.52	0.86	1.05	0.53	0.83	1.3	0.64	1.6	0.93	0.74	0.59	0.43	0.75	1.45	0.7	-	-		. 0.71	1.14	1.03	0.52
0.54	0.92	0.47	0.51	1.29	1.29	1.29	1.29	0.47	0.74	1.03	0.45	0.5	0.59	2.11	0.43	0.67	1.47	0.26	0.81	1.51	0.95	1.07	. 0.57	0.56	2.22	1.11	0.72	0.35	1.72
0.73	0.87	0.75	0.35	1.23	1.23	1.23	1.23	0.8	1.86	0.38	0.51	1.42	0.58	0.41	2.21	1.12	0.3	0.67	1.48	0.69	1.82	0.53	0.55	0.79	0.27	0.89	1.59	1.43	0.27
1.51	0.84	0.62	0.37	0.81	0.81	0.81	0.81	1.05	2.25	0.4	0.64	1.32	0.77	0.42	1.18	1.31	0.36	0.77	0.94	0.75	1.16	0.69	0.78	0.83	0.31	98.0	1.01	1.94	0.34
1.19	0.73	1.13	0.42	1.06	1.06	1.06	1.06	0.91	0.85	9.0	0.49	0.32	0.49	29.0	0.74	1.27	0.62	0.49	0.57	0.97	0.84	0.62	1.31	0.79	0.72	0.81	1.48	0.73	0.59
0.76	0.78	0.61	0.68	0.74	0.74	0.74	0.74	0.79	0.5	1.08	1.25	0.51	0.79	1.14	0.53	0.64	1.16	0.31	1.04	0.78	0.43	0.67	0.6	1.06	0.99	0.73	0.8	0.31	2.31
0.67	0.82	0.64	0.69	1.19	1.19	1.19	1.19	0.75	0.59	0.98	1.06	0.53	0.7	0.75	0.55	0.59	1.33	0.29	1.13	0.81	0.4	0.64	0.52	0.9	1.35	0.8	0.79	0.16	0.98
GAD1 vGAD67	OXTR	IL2RB	SSBP1	CHAT VN	HAT WIT	CHAT vN2	CHAT vR	IL 10RB	PLA2G1B	ICAM2	MGST3	INSR	HLA-A	EMR3 v1	SLC6A14	117	PDGFRA	KLK1	GNRH1	HRH3	CARD10	NR6A1 v1	ZFP36L1	PREB	RTN3	CYP4F8	STX1A	BRE	CTSW
0.86333333	0.85555556			闷	0.85 CHAT	0.85	0.85	0.84944444		0.84333333	0.841666667			-		0.831666667				0.81777778	2		0.81444444	0.81277778		0.80555556		0.79777778	0.783333333
0	0		0					0		0	0		0	0	0	0				0									

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1.13	0.69	0.96	1.69	0.46	0.46	0.46	0.46	0.75	0.54	0.63	0.89	0.37	1.06	0.55	0.63	0.73	0.84	2.01	0.51	0.63	0.33	1.04	1:1	0.43	0.23	0.78	0.4	0.44	0.29
1:11	0.76	0.71	1.43	0.55	0.55	0.55	0.55	0.51	0.47	1.21	0.99	1	0.92	0.94	0.48	0.97	0.68	1.26	0.85	0.97	0.47	1.1	1.09	0.61	0.28	0.68	0.45	0.69	0.32
0.89	1.08	0.94	1.23	9.4	0.4	0.4	0.4	0.52	0.72	0.74	99.0	0.82	1		0.57	0.93	0.62	1.6	0.32	0.45	0.63	1.12	1.19	0.56	0.26	0.8	0.4	0.84	0.29
0.86	1.04	0.86	0.95	0.49	0.49	0.49	0.49	0.8	0.36	1.16	0.67	99.0	0.58		9.0	0.63	0.57	1.25	0.51	0.75	0.62	1.18	0.86	1.01	0.37	0.79	0.36	0.64	0.51
1.24	0.86	0.82	1.94	0.44	0.44	0.44	0.44	0.9	0.58	-	0.89	0.72	1.01	98.0	9.0	0.7	0.92	1.69	0.67	9.0	0.48	0.87	0.91	0.57	0.51	0.8	0.44	0.62	0.36
0.76	0.56	96.0	1.37	0.98	0.98	0.98	0.98	0.62	0.49	0.62	0.79	0.86	1.18	0.54	0.57	0.52	0.81	1.39	0.5	0.85	0.7	0.92	1.08	0.42	2.14	0.72	0.65	0.75	0.41
0.78	0.68	1.06	0.57	1.25	1.25	1.25	1.25	0.93	1.41	0.78	0.47	1.67	0.71		1.17	0.84	0.79	0.56	1.17	0.72	1.68	0.61	0.82	0.61		0.77	1.05	1.62	0.32
0.65	1.1	0.56	0.58	0.83	0.83	0.83	0.83	0.98	0.67	0.75	1.11	0.84	0.9	0.94	0.47	96.0	0.81	0.29	0.76	1.09	0.59	0.89	0.54	1.18	0.85	1.13	0.95	0.32	2.88
0.69	-1.19	0.68	9.0	0.51	0.51	0.51	0.51	1.1	0.67	0.88	1.5	1.16	0.87	0.58	0.68	0.85	0.67	0.37	0.97	0.79	0.52	0.85	0.5	1.37	0.73	0.83	0.76	0.32	=
0.74	0.76	0.48	0.8	0.85	0.85	0.85	0.85	ı	0.55	0.85	1.72	0.67	0.68	1.11	0.56	0.67	1.12	0.32	0.82	0.92	0.41	0.57	0.37	1.24	6.0	0.72	0.7	0.19	0.65
0.58	. 0.65	1.69	.0.57	1.1	1.1	1.1	1.1	. 0.89	1.09	1.04	0.53	0.87	0.92	· .	1.42	0.64	1.03	0.69	1.3	. 0.69	1.19	9.0	0.87	9.0		. 0.57	69:0	. 1.88	0.34

			_	_				Γ-	_	_	_	_	_	Τ_	_										Γ-	_			
0.92	0.83	0.68	0.65	0.27	0.24	0.24	0.48	0.39	0.39	1.34	0.38	0.38	0.5	0.75	0.79	0.55	0.74	0.21	0.73		0.52	0.93	0.54	1.14		0.73	0.57	0.47	0.53
1.58	0.52	0.77	1.44	0.22	0.38	0.38	0.93	0.55	0.55	0.3	99.0	0.79	0.56	0.68	0.8	0.54	0.92	0.61	1.16	0.19	1.27	0.74	0.79	0.3	0.65	0.35	0.39	1.57	0.54
-	0.8	0.34	0.62	0.17	0.41	0.41	0.52	0.33	0.33	1.93	0.79	0.47	0.83	0.54	0.56	0.88	0.99	0.33	1.91	0.03	0.5	0.49	0.65	1.06	0.05	0.58	1.02	0.71	0.73
0.86	1.38	0.49	0.59	0.19	0.28	0.28	29.0	0.38	0.38		0.85	0.63	0.82	0.45	0.65	0.74	1.1	0.7	1.15	0.02	0.45	. 0.62	0.89	98.0	0.04	0.85	1.43	9.0	0.82
0.86	1.37	0.69	1.23	0.39	0.19	0.19	0.54	9.0	9.0	0.85	0.68	0.83	0.85	1.35	0.77	0.64	1.25	9.0	0.4	0.09	1.18	0.79	1.24	0.58	0.16	0.79	0.73	0.59	1.55
0.95	0.69	0.82		0.25	0.3	0.3	0.83	0.62	0.62	0.34	0.77	1.27	0.58	0.74	0.91	99.0	0.71	0.78	0.62	0.1	0.63	0.61	99.0	0.42	0.63	0.58	0.43	0.83	9.0
0.95	0.57	0.69	1.23	0.24	0.33	0.33	0.56	0.49	0.49	0.36	0.63	0.96	0.5	0.89	0.98	0.61	0.47	0.55	0.57	0.13	0.95	0.95	0.62	0.46	0.71	0.4	0.34	0.7	0.51
MC3R	HTR38	NR1H3	L12B	SERPINA6	CNTFR v1	CNTFR v2	PNMT	TCIRG1 v1	TCIRG1 v2	PTX3	MC1R	BCL2L2	EP0	HOXB1	ETS1	MADA	PF4	IGF2	6900	COSE	I ICAM3	FUS	PRLR	HSP105B	TLR6	NROB2 ·	SIGLEC6	PTGDS	
0.778888889	0.773888889	0.766111111	0.763333333	0.76277778	0.756111111	0.756111111	0.748333333	0.74222222	0.74222222	0.741176471	0.73944444	0.736666667	0.73555556	0.735294118	0.723888889	0.723888889	8 <i>TTTTT</i> 117.0	0.716111111	0.71222222	0.711333333	0.70944444	0.705	0.70444444	0.70111111	0.700588235	0.69722222	0.691666667	0.690555556	· 0.69 MAOB

0.41	0.66	0.87	0.54	1.01	2.1	2.1	0.7	0.85	0.85	0.49	0.69	0.61	0.88	0.69	0.78	- 0.76	0.39	0.85	0.34	1.72	0.83	0.37	0.45	0.77	0.56	10.1	0.75	0.72	0.7
0.77	0.73	1.43	0.34	1.45	1.59	1.59	1.07	1.6	1.6	0.39	0.57	0.67	0.82	0.58	0.4	. 0.54	0.62	0.94	0.46	1.62	0.59	0.42	1.12	0.96	0.43	9:0	0.9	0.69	0.64
0.49	0.63	0.83	0.72	1.4	1.35	1.35	1.29	0.86	0.86	0.53	1.13	0.55	1.15	0.77	0.71	0.69	0.42	0.95	0.42	1.83	0.48	0.46	0.53	0.68	. 0.56	0.84	0.72	0.55	0.87
0.58	0.74	0.79	0.63	2.76	1.5	1.5	0.99	2.28	2.28	0.72	1.24	0.69	1.02		9.0	0.97	0.42	1.57	0.36	2.31	0.69	0.57	0.78	0.81	4.95	1.05	0.85	0.56	0.57
0.5	0.53	1.05	0.46	1.52	1.57	1.57	0.88	0.91	0.91	0.54	29.0	0.81	0.92	9.0	0.68	99.0	0.48	1.17	0.58	2.15	0.7	0.57	0.52	96.0	0.62	0.88	0.82	0.87	0.7
0.36	0.62	0.96	0.69	2.6	1.58	1.58	0.78	1.44	1.44	0.91	9.0	0.62	0.94	0.69	0.67	0.63	1.09	1.65	0.34	0.24	0.83	0.72	0.78	0.72	0.48	0.85	0.72	0.64	0.51
0.54	0.77	9.0	0.61	0.29	0.26	0.26	0.33	0.34	0.34	1.29	0.32	0.55	0.41	0.86	0.71	0.49	0.93	0.21	1.2		9.0	1.23	0.74	0.86	0.41	0.49	0.53	0.36	0.54
1.02	0.84	0.68	0.79	0.23	99.0	99.0	0.91	0.5	0.5	0.4	1.04	1.05	0.68	0.47	0.81	0.82	0.72	0.72	0.58	0.08	0.8	0.43	0.68	0.34	0.47	69.0	0.58	0.72	0.78
0.85	0.87	0.64	0.61	0.26	0.33	0.33	0.83	0.54	0.54	0.43	1.16	0.95	0.73	0.51	0.83	1.64	0.51	0.8	0.68	0.07	0.54	0.58	0.67	0.57	0.62	0.81	0.68	0.74	0.56
0.76	0.75	0.77	0.9	0.21	0.3	0.3	0.74	0.41	0.41	0.46	0.73		0.58	0.8	0.7	0.78	0.55	0.68	0.55	0.09	0.58	0.5	0.5	0.33	0.48	0.51	0.52	0.75	0.73
0.62	0.63	. 0.63	0.69	0.27	0.24	0.24	0.42	0.27	0.27	1.32	0.4	0.43	0.47	1.13	0.68	0.43	9.0	0.27	0.77	÷	0.63	1.71	0.52	0.8	0.09	0.54	.0.47	0.36	0.54

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0.4	0.77	0.47	0.72		0.54	0.61	0.71	0.44	0.32	99.	0.63	0.63	0.63	0.59		0.47	55.	0.26	0.42	42	1.18	0.88		0.52	0.69	0.8	ا	0.39	0.35
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0.5	0.72	1.47	0.8	0.23	0	0.53	189		9:	0.4	2	12:	1:0	89	5.	-	0.8	0.8	1.23	1.7	0.3	9.0	2	0.3	0.3	0.7	0.7	0.6	0.4
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0.48	1.18	0.38	1.0	9.0	8	0.36	0.54	26	0.07	7	6	7.7	7.7	1.78	2	24	15	12	0.22	22	53	0.67	0.4	14.	61	8	33	0.25	24
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0.61	1.3	0.41	0.56	0.0	9.	0.4	0.74	7.	0.05	0	0.59	.50	55.	120	<u> </u>	0.9	4.	S.	0.3	o	1.13	386	2	1.93	99	<u>8</u>	7,4	0.25	0.22
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0.55	99	54	38	0.32	<u>.</u>	0.94	-	0.37	0.18		0.65	0.65	65	1.11	44	63	99	3	1.01	01	54	35	56	37	55	29)3	79	39
0	0	0	o	0	7	Ö		Ö	0		0.	0	0.		0.	Ó.	0	o	-	1.	0	0.	0	0	õ	0.7	1.0	0	ဝ
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0.72	0.64	0.86	0.48	0.1	0.54	0.75	0.69	9.0		0.56	0.76	1.76	7.	142	3.	1.78	.62	.91	0.98	36.	0.7	0.56	0.7	0.41	.49	.72	.6£	0.62	ري
19	٦	0	٥		0	0	J			0	٥	0	0	0	0	0	0	0	0	0		0		0	0	0	0	0	9
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2	ജ	82	14	19	12	0.6	0.7	5	36	82	78	/8	8	5	5	œί	32	33	32	32	3.	8	13	15	4	12	3	0.6	g:
0.62	0.33	0.88	0.44	0.19	0.42	0	0	Ō	0.96	0.5	0	0	0.7	0.7	0.	0	0.6	0.0	0.82	0.8	0	0.58	0.7	0.	0.4	0.72	0.5	0	82.0
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0.68555556 C1QBP	0.68444444 CCL28	딠	9	CHRNA6	ICFBP3	ADAM8	CCL27	TB4R	GFBP6	贸	0.663888889 SR-BP	SR-BP1	0.663888889 SR-,BP		0.659333333 ADRBK	100559	\equiv	IL 20RA	ICAM4 v	0.64055556 ICAM4 v2	낊	احر	7	اع		SLC25A3	ଧ	낅	PTP SS PTS
등	덩	PIAS	0.68 RFX2	푕	띵	Ş	덩	巴	띵	0.668823529 ADRB	슳	쏬	섫	읆	칡	잉	0.65555556 PTPN	ŭ	3	3	0.639444444 CCBP;	0.63777778 BATE	0.633529412 ZNF14	IL8Ra	0.630588235 1F130	띯	GPR2	NEK3	닭
등	듺		<u>~</u>	픐	2			_		긁	뜴	픐	씘		읈		믌		2	=	픩	믌	끍		5	쑮			븨
15	#	0.68277778	9	0.676	0.675882353	0.673888889	0.673888889	0.66944444	0.6688888889	긼	8	8	齒	0.660555556	2	0.65777778	诏	0.641666667	0.640555556	S)	\$	E	#1	22	23	0.628888889	0.62222222	0.621666667	=
띯	<u>₹</u>			0	떯	器	器	144	器	2	器	器	器	汉	3		띯	99	35	띯	4		8	22	8	器	2	9	=
	첧	123			巡	巡	2	36	떯	器	떬	贸	뛵	띯	뗈		띯	3	<u>왕</u>	흾	쫤	闫	뙸	32	뙶	器	띪	읦	0.62111111
9.0	9.0	0.6			9.	9.	9.	9.6	9.	9	9	9	9	9	<u>@</u>	[2]	9	.6	9.	9	ر افع	얼	9	9	9	9	2	9	9
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FIG.11-18B

0.76	0.41	0.63	0.58	1.37	0.72	0.73	0.68	0.95	0.63	0.85	0.47	0.47	0.47	0.37	0.58	0.41	0.86	0.87	0.54	0.54	0.28	0.63	0.56	0.32	0.85	0.38	99.0	0.82	0.39
1.27	0.53	0.47	98.0	2.33	0.61	0.87	0.49	0.59	0.48	0.78	9.0	9.0	9.0	0.31	0.92	0.38	0.84	9.0	0.51	0.51	0.3	0.57	0.66	0.3	0.63	0.48	0.61	0.74	0.79
0.77	0.36	9.0	0.39	1.66	0.68	0.9	0.64	1.72	0.61	0.69	0.7	0.7	0.7	0.23	0.97	0.35	1.01	0.99	0.57	0.57	0.34	0.56	0.63	0.37	0.82	0.24	0.84	0.96	0.73
0.79	0.32	0.44	0.9	1.54	0.97	0.8	.0.57	0.99	0.99	0.62	0.77	0.77	0.77	0.29	1.01	0.56	0.57	0.9	0.55	0.55	0.66	0.44	0.87	0.59		0.41	0.65	0.9	0.96
0.89	0.36	0.57	0.94	1.74	0.83	0.81	0.5	0.54	0.62	1.19	0.64	0.64	0.64	0.52	0.99	0.51	•	0.69	0.55	0.55	0.41	0.51	0.77	0.33	0.71	0.53	0.52	0.85	1.56
1.07	0.24	0.65	0.75	0.31	0.61	0.88	0.64	0.64	0.98	0.75	0.45	0.45	0.45	0.3	1.1	0.33	0.95	1.01	0.87	0.87	0.68	0.54	0.61	9.0	0.97	0.39	0.94	0.72	1.05
0.4	1.12	0.37	0.97		0.63	0.63	0.71	0.32	0.18	0.81	0.39	0.39	0.39	0.95		0.39	0.52	0.19	0.45	0.45	1.17	0.9	0.54	0.55	0.52	0.65	0.38	0.35	0.65
0.72	0.67	1.12	0.62	0.09		0.26	0.75	0.89	0.99	0.68	0.92	0.92	0.92	0.4	0.77	0.77	0.59	1.24	0.63	0.63	0.27	0.51	0.52	0.72	- 0.43	0.8	0.77	0.78	0.23
0.65	0.79	0.59	0.61	0.07	0.67	0.53	0.79	0.51	0.54	0.71	0.54	0.54	0.54	0.63	0.58	0.48	0.42	0.68	0.48	0.48	0.27	0.57	0.61	0.71	0.56	0.61	0.61	0.62	0.3
0.73	0.9	1.22	0.77	0.11	0.44	0.61	0.57	0.82	1.26	0.73	0.71	0.71	0.71	0.5	0.41	-	0.44	0.75	0.95	0.95	0.31	0.39	0.74	0.57	0.55	0.95	0.61	0.53	0.82
0.4	0.88	0.62	0.4		0.59	0.62	0.57	0.54	0.27	0.89	0.57	0.57	0.57	0.48		0.38	0.54	0.5	0.45	0.45	1.49	0.78	0.77	0.44	0.83	0.89	0.48	0.33	0.62

WO 2004/108899 PCT/US2004/017686

61/126

0.67	0.41	0.5	.73	57	66	47	39	0.49	58	0.6	36	<u>85</u>	8	14.	14	.53	36	48	.48	88.	.56	.33	.82	88	0.58	17	34	0.17
0	0		0	0	0	0	O	0	0		0	0	0	0	0	0	0	Ö	0		0	o	0	Ö	0		0	0
0.7	0.79	0.89	0.61	0.48	0.46	1.63	0.59	0.44	0.82	0.57	1.4	0.57	0.57	0.53	0.53	0.54	0.48	0.95	0.95	0.52	0.91	0.28	0.87	1.19	0.73	0.55	0.94	1.31
0.66	0.26	2.49	0.51	0.63	0.16	0.32	0.97	9.0	1.16	0.56	0.15	0.05	0.05	0.19	0.19	0.15	0.34	2.03	2.03	0.34	0.39	9.0	0.33	0.5	0.67	0.74	0.23	0.09
0.8	0.13	1.73	99.0	0.83	0.25	0.31	1.49	0.93	0.72	0.79	0.16	0.04	0.04	0.13	0.13	0.13	0.15	1.41	1.41	0.22	0.29	0.82	0.35	0.47	0.65	0.85	0.27	0.04
0.87	0.52	0.43	1.3	0.83	0.53	0.61	0.44	0.51	0.71	1.1	0.39			0.54	0.54	0.29	0.44	0.54	0.54	0.86	0.61	0.46	0.46	0.5	0.78	0.72	0.59	0.19
0.77	0.97	0.15	0.83	0.76	0.32	96.0	0.49	0.36	0.38	0.48	0.85	0.83	0.83	0.72	0.72	0.78	0.32	0.28	0.28	0.38	0.62	0.43	0.85	0.65	0.77	0.72	0.68	1.2
0.58	0.92	0.16	0.88	0.8	0.41	1.02	0.68	0.32	0.29	0.51	0.83	0.56	0.56	0.51	0.51	0.33	0.26	0.27	0.27	0.52	0.57	0.39	0.78	0.65	0.46	0.62	0.59	1.18
FOXP3	IRHR	MAPK1	KLF16	4K1	N.	NGFB	11	.5R	8100	TOLLIP	1F6	GR3A	FCGR3B	HR1 .	HRZ	RA3	~	X1 v1	X1 v2)1E		PR49	A	STAT5A	CYP2J2	IM1	SP1 v1	11.3
0.615294118 FC	~~	0.6061111111 M/	0.603529412 KL	0.603333333 IRAK			0.601111111 1511	0.59944444 MC5R	0.598888889 CC	0.59722222 TC	0.597058824 11.1	0.596875 FCGR3A	0.596875 FC	0.59444444 CRHR1	0.59444444 CRHR2	0.59055556 CFRA3	0.59 [8	0.588888889 NFX1	0.58888889 NFX		0.58722222 C2	0.583333333 GPR49	0.583333333 IL1A	0.583333333 ST	0.58222222 CY	0.57777778 GRM1	0.576666667 MASP	0.56944444 NFI

FIG.11-19A

SUBSTITUTE SHEET (RULE 26)

FIG.11-19B

0.32	0.87	0.32	0.45	0.42	1.39	0.4	0.42	0.65	0.5	0.53	0.66	0.71	0.71	0.82	0.82	0.67	1.04	0.3	0.3	0.48	0.43	9.0	0.32	0.55	0.48	0.43	0.57	0.52
	0.59	0.54	0.37	0.45	0.78	0.21	0.39	0.89	99.0	0.47	99.0	0.82	0.82	0.94	0.94	0.87		0.51	0.51	0.56	0.5	0.97	0.52	0.4	0.3	0.52	0.91	0.39
0.29	0.63	0.27	0.43	0.38	1.17	0.36	0.32	0.98	0.46	0.57	0.32	0.91	0.91	-:	-:	0.58	0.5	0.26	0.26	0.44	0.48	0.53	0.72	0.59	0.34	0.41	0.58	0.5
0.31	0.53	0.69	0.26	0.58	0.59	0.27	0.35	1.06	0.54	0.64				1.17	1.17	0.91	0.43	0.32	0.32	0.42	0.84	1.07	0.84	0.51	0.67	0.46	0.85	0.3
0.33	0.57	0.39	0.24	0.56	1.07	0.25	0.49	0.73	0.71	0.4	0.7	1.07	1.07	0.66	99.0	1.05	0.37	0.41	0.41	0.61	0.35	0.99	0.63	0.5	0.4	0.55	0.7	0.45
0.54	0.63	0.44	0.37	0.45	0.85	0.23	0.36	0.59	0.49	0.83	0.64	0.59	0.59	1.08	1.08	0.64	0.32	0.55	. 0.55	0.72	0.98	0.7	0.58	0.51	0.53	0.43	0.7	0.3
0.55	9.0	0.78	0.78	0.71	0.65	0.51	0.85	0.26	0.65	0.68	0.33	0.05	0.05	0.17	0.17	0.48	1.61	0.89	0.89	1.03	0.34	0.36	0.46	0.28	0.48	0.46	0.41	0.19
1.01		0.27		0.61	0.3	0.93	0.45	9.0	0.5	0.46	0.8	0.86	0.86	0.62	0.62	0.33	0.73	0.3	0.3	0.26	0.8	0.53	0.36	0.95	0.79	0.83	0.57	1.17
0.82	0.75	0.38	99.0	0.71	0.35	0.79	0.57	0.48	0.69	0.41	0.46	1.15	1.15	0.65	0.65	0.41	0.61	0.34	0.34	0.23	0.59	0.61	0.57	9.0	0.9	1	0.53	1.14
0.73	0.72	0.22	0.62	0.58	0.28	1.09	0.58	0.54	9.0	0.4	1.04	1.13	1.13	0.49	0.49	0.43	1.54	0.28	0.28	0.33	. 0.57	0.5	0.38	0.83	0.57	0.64	0.53	0.95
0.51	0.57	0.26	0.56	0.51	0.59	0.47	0.73	0.36	0.32	0.75	0.4	0.12	0.12	0.24	0.24	1.51	0.53	0.48	0.48	1.58	0.74	0.33	99.0	0.44	0.38	0.3	0.39	0.16

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0.14	0.97	0.15	0.15	0.48	0.34	0.59	0.59	0.37	0.41	0.33	0.37	0.65	0.59	0.72	0.32	0.61	0.56	0.34	1.24		0.46	0.36	0.44		0.75	0.83	9.0	0.29	0.66	0.25
0.35	0.47	0.17	0.17	0.5	0.69	0.3	0.33	0.36	99.0	2.35	1.03	0.81	0.4	0.43	0.93	0.59	0.23	0.76	0.54	1.18	0.45	0.93	0.38	0.44	0.61	0.75	0.39	0.7	0.57	0.33
0.12	0.87	0.12	0.12	0.46	0.45	0.79	0.45	0.42	0.25	0.17	0.19	0.41	0.71	1.15	99.0	0.59	0.45	0.59	0.5	0.23	0.84	0.46	0.38	0.49	0.48	0.38	0.9	0.38	0.63	9.0
0.21	0.94	0.09	0.09	0.47	0.45	9.0	0.26	0.41	0.37	0.18	0.33	0.36	0.93	1.39	0.61	0.7	0.55	0.39	0.56	0.24	. 1.23	0.54	0.46	0.49	0.34	0.38	0.72	0.34	0.74	1.26
0.3	1.34	0.11	0.11	0.79	0.49	0.71	0.37	0.15	0.47	0.37	0.58	0.44	0.72	9.0	0.65	1	1.27	0.55	0.82	0.48	0.39	0.42	0.48	0.31	0.23	0.81	0.7	0.57	0.52	0.75
0.26	0.34	0.24	0.24	0.44	0.78	0.47	0.46	0.3	0.62	6.0	0.73	. 0.58	0.35	0.39	0.48	0.36	0.0	0.44	0.55	0.72	0.59	0.64	0.45	0.5	0.54	0.63	0.41	0.57	0.63	0.36
0.21	0.33	0.21	0.21	0.51	0.76	0.43	0.59	0.36	0.51	1.05	0.67	0.81	0.34	0.38	0.46	0.32	0.29	0.47	0.47	1.39	0.57	0.61	0.38	0.64	0.63	0.65	0.56	0.61	0.52	0.29
																													,	
CACNB3	CYPZE1	SYN1 vla	SYN1 vlb	PSPN	MPR1	AVPR2	BZM	TEC	HSPCA	MST1R	RORC	GH2 v2	FGF2	N0S2A v1	IGFBP2	LIRI	JAK1	VGF	HOXA1	NABR	HTRZA	PTGER4	SIGLECS	INFSF12 v1	PGRMC1	CD209L	PPYR1	11.14	CSR1	ESRRA
				830				0.548333333	_		0.541666667		\neg		\neg	<u>~</u>		\neg		0.534666667	_		<u></u>		12			2		0.52555556
0	0			0	0	Ö	0	0	0	O	0	O	Ö	Ö	Ö	O'	Ö	Ö	0	0	· O	·)	0	Ö	Ö	Ö	0)	o	Ö	0

yes yes yes

yes yes yes

yes yes yes yes yes yes

yes

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0.98	0.31	1.34	1.34	0.52	0.51	0.57	0.58	0.27	0.6	0.34	0.69	0.22	0.53	0.35	0.35	0.44	0.54	0.51	0.19	0.11	0.28	0.42	0.7	0.83	0.56	0.37	0.39	0.83	0.41	0.44
0.58	0.27	1.33	1.33	0.5	29.0	0.58	0.61	2.81	0.7	0.27	0.67		0.38	0.23	0.84	0.79	0.45	0.54	0.23	0.11	0.3	0.56	0.78	0.79	0.56	0.48	0.45	0.42	0.74	0.65
1.72	0.33	1.45	1.45	0.47		0.41	0.49	0.44	0.9	0.24	0.43	0.31	0.85	0.22	0.55	0.55	0.32	0.7	0.23	0.08	0.22	0.41	0.8	0.51	0.58	0.37	0.34	0.49	0.46	0.41
1.86	0.3	•		0.61	0.63	0.58	0.87	0.34	0.54	0.19	0.66	0.54	0.48	0.35	0.82	0.49	0.74	0.52		0.1	0.28	0.64	0.95	0.83	0.86	0.37	0.53	0.12	0.29	0.62
2.11	0.35	1.48	1.48	0.56	0.47	0.51	0.58	0.24	0.58	0.5	0.45	0.48	0.45	0.37	0.48	0.54	0.46	0.5	0.26	0.15	0.47	0.41	0.75		0.72	0.45	0.33	0.75	0.34	. 0.42
0.52	0.24	1.51	1.51	0.73	0.5	0.82	1.11	0.51	0.67	0.32	0.75	0.35	0.43	0.3	0.61	0.35	9.0	0.98	0.28	0.97	0.22	0.61	0.7	0.4	0.47	0.38	0.55	0.49	0.34	0.65
0.12	0.93	0.1	0.1	0.56	0.21	0.57	0.48	0.76	0.48	0.36	0.32	0.52	0.62	0.87	0.45	0.52	0.72	0.37	0.78		0.83	0.37	0.26		0.43	0.59	0.69	0.4	0.52	0.45
0.23	0.47	0.22	0.22	0.55	0.68	0.4	0.53	0.76	0.55	. 0.85	0.54	0.58	0.51	0.44	0.33	9.0	0.68	0.61	0.48	0.7	0.49	0.5	0.48	0.33	0.35	0.55	0.33	0.61	0.5	0.55
0.22	0.4	0.21	0.21	0.68	0.78	0.62	0.5	99.0	0.48	0.46	0.49	0.61	0.54	0.53	0.48	0.49	0.31	0.45	0.51	0.62	0.73	0.82	0.44	0.42	0.52	0.42	0.44	0.74	0.68	0.68
0.14	0.65			0.53	0.71	0.49	0.54	0.36		0.71	0.58	0.56	0.37	0.33	0.37	0.34	0.3	0.45	0.46	0.94	0.56	0.61	0.51	0.47	0.42	0.47	0.42	0.89	0.51	0.36
0.13	0.64	0.14	0.14	0.61	0.28	0.51	0.53	0.35	0.53	0.47	0.27	0.36	0.53	0.68	0.3	0.4	0.29	0.48	_		0.7	0.3	0.27		0.52	0.68	77.0	0.31	0.41	0.39

																								_			_	_	_
0.33	0.82	0.54	0.35	0.38		0.39	0.97	0.53	0.38	0.44	0.37	0.54		0.57	0.52		0.38	0.38	0.34	0.46	0.46	0.24	0.47	0.27	0.47	0.47	0.68	0.42	0.55
0.52	1.32	0.58	99.0	0.38	0.19	0.22	0.84	0.7	0.52	0.29	0.72	0.42	0.5	0.5	0.76	0.32	1.31	1.31	0.81	0.39	0.39	0.44	0.48	0.87	0.51	0.51	0.56	0.81	0.27
0.47	0.43	0.58	0.35	0.16	0.08	0.36	0.23	1.14	0.71	0.42	0.35	0.8	1.19	1.09	0.23	0.76	0.29	0.29	0.3	0.63	0.63	0.29	0.62	0.27	0.68	0.68	0.39	0.55	0.46
0.86	0.41	0.67	0.45	0.18	0.09	0.37	0.15	6.0	0.8	0.5	0.35	1.21	1.23	1.13	0.21		0.49	0.49	0.22	0.41	0.41	0.26	0.68	0.25	0.61	0.61	0.4	0.56	0.46
9.0	1.59	0.86	1.17	0.27	0.12	0.3	0.58	0.39	0.66	0.65	0.48	0.77	0.35	0.59	0.38	0.57	0.56	0.56	0.45	0.56	0.56	0.2	0.5	0.55	0.64	0.64	0.5	0.24	0.58
0.52	0.53	0.43	0.51	0.33	0.12	0.5	0.61	0.27	0.52	0.4	0.46	0.34	0.56	0.36	0.74	0.51	0.45	0.45	0.61	0.33	0.33	0.4	0.48	0.62	0.28	0.28	0.42	0.67	0.51
0.41	0.7	0.36	0.55	0.44	0.14	0.33	0.77	0.24	0.44	0.41	0.65	0.32	0.73	0.4	0.54	0.38	0.53	0.53	0.63	0.32	0.32	0.41	0.31	0.46	0.37	0.37	0.45	0.79	0.51
			,																										
NFKBIB	HMOX1	BTN3A1	WISP2	PTPNS1	PTN	NRG1 VGGFZ	RINZ	11.3	MS4A6A v2	0.51 PILR(BETA)	MAGED1	/ GRM5	PLA264A	SLC15A2	IRF2	TACR2	ILF3 v1	ILF3 v2	0.5 CABBR1 v3	GAB2 v1	GAB2 v2	MS4A3	11.18	POMC	XCL1	XCL2	MF	11.20	FCER2
0.523333333	0.522 <i>7777</i> 78 HMOX	0.521666667	0.52055556 WISP2	0.516666667	0.516 PTN	0.513529412	0.51222222	0.511666667	0.510555556	0.51	0.508333333 MAGED	0.506666667	0.506666667	0.506111111	0.50444444 IRF2	0.502142857	0.500588235	0.500588235	0.5	0.49777778 GAB2 v	0.49777778 GAB2	0.49777778 MS4A3	0.496666667	0.496111111	0.493888889 XCL	0.493888889	0.493333333	0.49222222	0.490555556
				,																							·		

0.51	0.13	0.47	0.56	96.0	0.98	0.84	0.17	0.35	0.32	0.85	0.4	0.38	0.14	0.19	0.6	0.37	0.44	0.44	0.46	0.67	0.67	0.43	0.29	0.5	0.46	0.46	0.51	0.43	0.5
0.59	0.1	0.27	0.4	0.78	0.98	0.78	0.15	0.36	0.56	0.45	0.64	0.37	0.17	0.24	0.31	0.43	0.39	0.39	0.68	0.83	0.83	0.52	0.33	0.69	0.57	0.57	0.45	0.27	0.48
0.55	0.14	0.64	0.58	0.87	0.79	0.85	0.14	0.64	0.52	0.49	0.41	0.52	0.13	0.25	0.49	0.32	0.48	0.48	0.68	0.45	0.45	0.52	0.38	0.69	0.61	0.61	0.57	0.35	0.46
9.0	0.17	0.42	0.45	0.7	1.97	0.85	0.19	0.55	0.54	0.77	0.62	0.37	0.14	0.56	0.65	0.63	0.56	0.56	0.7	0.69	0.69	79.0	0.51	0.56	1.0	0.77	0.48	0.24	0.53
0.68	0.14	0.64	0.32	1.1	1.57	0.61	0.18	0.55	0.47	0.58	0.56	0.3	0.17	0.3	0.51	0.52	0.33	0.33	0.53	0.49	0.49	0.47	0.53	9.0	0.61	0.61	0.56	0.55	0.38
0.51	0.23	0.65	99.0	1.01	0.31	0.59	0.5	0.32	0.4	0.7	0.29	0.33	0.62	0.25	0.52	0.7	0.92	0.92	,	0.75	0.75	9.0	0.35	0.69	0.7	0.7	0.67	0.49	0.59
0.36	0.53	0.51	0.33	0.34		0.38	0.76	0.57	0.4	0.44	0.33	0.46		0.87	0.38		0.53	0.53	0.22	0.56	0.56	0.15	0.51	0.3	0.49	0.49	0.58	0.52	0.54
0.51	0.47	0.49	0.63	0.29	0.14	0.53	0.73	0.63	0.58	0.42	0.73	0.55	0.54	0.34	0.46	0.51			0.53	0.29	0.29	0.57	0.49	0.42	0.16	0.16	0.4	0.07	0.43
0.63	0.64	0.4	0.53	0.39	0.15	0.41	0.65	0.39	0.57	0.64	0.56	0.44	0.67	0.54	0.57	0.58	0.27	0.27	0.51	0.32	0.32	2.09	1.02	0.38	0.32	0.32	0.29	0.38	0.46
0.4	0.38	0.37	0.43	0.3	0.11	0.42	0.91	0.32	0.49	0.47	0.79	0.59	0.46	0.35	0.77	0.43	0.35	0.35	0.54	0.26	0.26	0.55	0.35	0.5	0.37	0.37	0.41	0.73	0.38
0.37	0.68	0.51	0.44	0.42			0.39	0.36	0.31	0.29	0.44	0.41		0.58	0.44		0.23	0.23	0.29	0.55	0.55	0.15	0.64	0.31	0.27	0.27	0.56	0.79	0.74

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0.31	0.37	0.71	0.64	0.45	0.59	0.37	0.36	0.43	0.27	0.44	0.34	0.34	0.54	0.31	0.56	0.37	0.3		0.3	0.38	0.33	0.57	0.21	0.37	0.32	0.08	0.69	0.46	0.32
0.43	0.98	0.48	0.53	0.43	0.69	0.42	-	9.0	1.7	0.61	0.71	0.86	0.45	0.35	0.33	0.58	0.39	0.56	0.81	0.42	0.36	0.25	1.04	0.26	0.48	0.19	0.33	0.59	0.25
0.48	0.34	0.51	0.7	0.65	0.36	0.22	0.53	96.0	0.16	0.3	0.18	0.53	0.19	0.26	0.33	0.58	0.32	0.32	0.32	0.26	0.23	0.51	0.11	0.25	0.17	0.04	0.14	0.31	0.14
0.57	0.28	0.51	0.22	0.74	0.37	0.27	0.53	1.16	0.22	0.3	0.25	0.45	0.2	0.2	0.37	0.45	0.4	0.35	0.31	0.17	0.21	0.57	0.1	0.46	0.24	0.04	0.31	0.34	0.18
0.43	0.32	0.61	0.28	0.94	0.7	1.78	0.65	0.23	0.24	1.18	0.63	0.59	0.26	0.35	99.0	0.77	0.37	0.77	0.4	0.75	0.24	0.45	0.18	0.34	0.55	0.1	0.36	9.0	0.26
0.49	0.62	0.4	0.59	0.49	0.5	0.43	0.59	0.48	0.64	0.7	0.48	0.49	0.54	0.5	0.5	0.34	9.0	99.0	0.31	.0.36	0.37	0.45	0.51	0.73	0.55	0.11	0.38	0.45	0.27
0.48	0.51	0.41	0.49	0.36	0.77	0.4	0.58	0.52	0.7	9.0	0.54	0.43	0.42	0.44	0.49	0.32	0.62	0.54	0.39	0.39	0.37	0.57	9.0	0.51	0.35	0.13	0.5	0.45	0.2
MAP3K3	PRL	LCN7	CIOT-2	BAX vB	ncn	SYN2 v lia	PNR	CBP2	CST7	ITGA2	S0CS3	CACNA1B	PNOC	E124	IL 1RAPL 1	ADRA1A v1	HSPA8 v1	HSPB7	GSR	FLJ12541	CX3CL1	IL 1R2	IL 1RAPL2	NR3C2	IL 10RA	WNT1	PPIA	ADORA2A	CCL14 v1
0.490555556 MAP3K3	0.49 PR	0.48944444	0.485 GIOI - 2	0.484705882 BAX	0.48444444 UCN	0.482352941	0.481666667	0.48 GBP2	0.47944444 CST	0.47888888 ITGA2	0.478888889 SOCS.	0.478333333	0.476470588 PNOC	0.475	0.47277778 IL1RAPI	0.472352941 ADRA1A	0.47222222 HSPA8	0.470714286 HSPB	0.468333333 CSR	0.46777778	-	0.46277778	0.461666667		0.453333333	0.45055556 WNT	0.448333333	0.44777778 ADORA2A	0.44777778
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FIG.11-22B

0.62	0.44	0.4	0.77	0.33	0.44	0.52	0.34	0.14	0.2	0.5	0.66	0.42	0.49	0.74	0.52	0.45	0.49		9.0	1.3	0.52	0.4	0.65	0.49	0.7	0.45	0.39	0.45	1.13
0.55	0.54	0.69	0.48	0.56	0.46	0.49	0.22	0.16	0.22	0.24	0.58	0.58	0.38	0.66	0.38	0.48	0.76	0.36	0.56	0.33	1.02	0.83	0.56	0.46	0.47	0.89	0.5	0.56	0.77
0.47	0.52	0.42	0.64	0.46	0.22	9.0	0.35	0.16	0.25	0.21	9.0	0.41	0.41	0.61	0.57	0.75	0.51	0.09	0.81	6.0	0.39	0.32	0.4	0.4	0.77	0.64	0.68	0.47	0.84
0.52	99.0	0.7	0.59	0.35	0.12	0.33	0.33	0.23	0.14	0.3	0.47	0.52	0.85	0.57	0.53		0.69	0.2	0.68	0.55	0.58	0.31	0.43	0.47	0.45	2.77	1.17	0.57	.0.57
0.58	0.44	0.44	0.56	0.46	0.53	0.37	0.26	0.16	0.23	0.28	0.55	0.42	0.56	0.73	0.51	0.49	0.63	0.15	0.64	0.31	0.64	0.34	0.79	0.38	0.45	0.71	0.58	0.5	0.85
0.57	0.37	0.4	0.44		0.29	0.48	0.28	0.33	0.25	0.73	0.51	0.53	0.5	0.81	0.5	0.47	0.58	1.08	0.53	0.46	1.43	0.5	0.69	0.36	0.48	1.55	0.48	0.39	0.76
0.51	0.29	0.5	0.55	0.34	0.52	0.57	0.49	0.88	0.14	0.32	0.37	0.4	0.37	0.7	0.42	0.42	0.39		0.33	0.28	0.26	0.52	0.12	0.39	0.23	90.0	0.36	0.49	0.32
0.47	0.75	0.36	0.38	0.52	0.56		0.55	0.45	1.29	0.53	0.5	0.32		0.55	0.5	0.45	0.34	0.5	0.4	0.43	0.39	0.39	0.54	0.44	0.99	0.1	0.19	0.34	0.24
0.5	0.48	0.38	0.43	0.44	0.45	0.3	0.47	0.55	0.99	0.77	0.39	0.51	0.87	0.5	0.5	0.42	0.42	0.48	0.38	0.45	0.4	0.36	0.36	0.53	0.43	0.11	0.78	0.35	0.28
0.42	0.48	0.29	0.38	0.43	0.57	0.32	0.65	0.52	0.83	0.55	0.53	0.45	0.71	0.53	0.46	0.32	0.38	0.53	0.32	0.22	0.36	0.36	0.87	0.77	0.32	0.07	0.22	0.29	0.23
0.43	0.43	9.0	0.56	0.29	0.58	0.33	0.49	0.68	0.16	0.36	0.33	0.36	0.36	0.24	0.38	0.37	0.31		0.34	0.49	0.29	0.63	0.15	0.56	0.21	0.07	0.31	0.45	0.45

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0.32	.0.32	0.32	0.21		0.56	0.53	0.19	0.48	0.48	0.4	0.52	0.15	0.15	0.29	0.29	0.4	0.36	0.32	0.31	0.62	0.7	0.38	0.37	0.31	0.33	0.16	0.35	0.59	0.31
0.25	0.25	0.25	0.36	0.34	0.34	0.39	0.41	0.32	0.32	0.79	0.31	0.78	0.78	0.22	0.51	0.31	0.76	0.35	0.26	0.54	0.57	0.61	0.7	0.27	0.22	0.43	0.33	0.19	0.35
0.14	0.14	0.14	0.13	0.2	0.38	1.11	0.16	0.61	0.61	0.25	0.7	0.17	0.17	0.37	0.45	0.57	0.35	0.7	0.29	0.2	1.24	0.3	1.87	0.26	0.11	0.1	0.22	99.0	0.44
0.18	0.18	0.18	0.19	0.17	0.45	1.47	0.16	0.39	0.39	0.39	0.71	0.12	0.12	0.55	0.38	0.52	0.34	0.18	0.32	0.15	0.73	0.31	1.11	0.24	0.07	90.0	0.16	0.47	0.58
0.26	0.26	0.26	0.46	0.22	0.54	0.33	0.21	0.29	0.29	1.08	0.48	0.37	0.37	0.27	0.57	0.57	0.77	0.43	0.24	0.39	0.33	0.63	0.39	0.22	0.18	0.16	0.28	0.25	0.39
0.27	0.27	0.27	0.48	0.16	0.32	0.36	0.27	0.33	0.33	0.5	0.39	99.0	99.0	0.31	0.23	0.26	0.48	0.34	0.49	95.0	0.22	0.53	0.09	0.35	1.23	0.47	0.39	0.3	0.34
0.2	0.2	0.5	0.41	0.23	0.35	0.41	0.38	0.33	0.33	0.45	0.37	0.65	0.65	0.19	0.41	0.07	0.47	0.29	0.5	0.75	0.13	0.48	0.08	0.26	0.27	0.63	0.47	0.28	0.3
CCL14 v2	CCL15 v1	CCL15 v3	.17R	FCER1G	LX49	IFNW1	CCL25 v1	PTGS1 v1	PTGS1 v2	TRAF1	WSX1	ACCN3 v1	ACCN3 v2	GABRE v3	RNASE3	RNPEPL1	FGF3	PTGIR	11.22	OF.	GRPR	HLALS	LRBA	SLC29A1	ITGAM	VDR	CDC37	ALDH7A1	HSPB2
0.44777778 C	0.44777778 C	0.44777778 C	0.446111111 11	0.446 F	0.445882353 G	0.445555556 IF		0.444705882 P	0.444705882 P	0.44444444 T	0.444117647 W	0.442 <i>77777</i> 8 A	0.442777778 A	0.441666667 G	0.44111111 R	0.43888889 R	_			0.432941176 0		0.42722222 H	0.427058824 L		_	0.424117647 V	0.421764706 C		0.419444444 H
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SUBSTITUTE SHEET (BI II E 26)

FIG.11-23B

1.13	1.13	1.13	0.34	0.85	0.62	0.16	0.91	0.38	0.38	0.35	0.35	0.54	0.54	0.49	0.39	0.44	0.29	0.52	0.67		0.18	0.42	0.11	0.46	0.26	0.94	0.68	0.44	0.4
0.77	17.0	0.77	1.08	0.87	0.47	0.16	0.86	0.48	0.48	0.24	0.34	0.42	0.42	0.49	0.46	0.76	0.38	0.45	0.44	0.22	0.34	0.25	0.2	0.49	0.45	0.53	0.5	0.54	0.55
0.84	0.84	0.84	0.44	0.89	0.75	0.15	0.81	0.52	0.52	0.39	0.38	0.59	0.59	0.63	0.76	0.43	0.46	9.0	0.47	0.24	0.23	0.37		0.59	0.46	0.55	0.78	0.4	0.32
0.57	0.57	0.57	6.0	0.87	0.52	0.26	0.78	0.57	0.57	0.38	0.49	0.51	0.51	0.91	0.42	0.56	0.37	0.89	0.48	0.3	0.47	0.26	0.13	0.8	0.43			0.75	0.25
0.85	0.85	0.85	0.59	0.85	0.48	0.23	0.82	0.45	0.45	0.36	0.41	0.44	0.44	0.61	0.41	0.57	0.32	0.58	0.61	0.24	0.29	0.36	0.15	0.55	0.41	0.78	0.65	0.51	0.28
0.76	0.76	0.76	0.87	0.37	0.44	0.2	0.75	0.43	0.43	0.56		0.59	0.59	0.85	0.69	0.56	0.4	0.54	0.55	0.26	0.39	0.5	0.14	0.66	0.64	0.69	0.76	0.47	0.42
0.32	0.32	0.32	0.24		0.34	0.78	0.21	0.31	0.31	0.43	0.49	0.14	0.14	0.21	0.33	0.4	0.41	0.31	0.28	0.65	0.67	0.34	0.74	0.18	0.21	0.5	0.35	0.36	0.85
0.24	0.24	0.24	0.38	0.21		0.25	0.34	0.63	0.63	0.43	0.39	0.62	0.62	0.3	0.5	0.34	0.45		0.37	0.51	0.35	0.63	0.36	0.42	0.7	0.35	0.26	0.27	0.41
0.28	0.28	0.28	0.49	0.22	0.34	0.34	0.28	0.59	0.59	0.34	0.46	0.49	0.49	0.63	0.45	0.38	0.36	0.77	0.51	0.62	0.38	0.44	0.31	0.66	0.13	0.42	0.28	0.46	0.65
0.23	0.23	0.23	0.3	0.24	0.37	0.32	0.27			0.32	0.26	0.55	0.55	0.41	0.38	0.32	0.45	0.31	99.0	0.59	0.22	0.47	0.19	0.53	1.84	0.46	0.28	0.28	0.42
0.45	0.45	0.45	0.16		0.31	0.57	. 0.2	0.45	0.45	0.34	0.5	0.18	0.18	0.22	0.31	0.44	. 0.42	0.31	0.35	0.52	0.3	0.41	0.32	·	0.21	0.26	0.43	0.34	0.29

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0.64	0.52	0.52	0.42	0.42	0.34	9.0	0.34	0.52	0.5	0.5	0.5	0.5	0.3	0.32	0.26	0.62	0.32	0.44	0.24	0.32	0.32	0.28	0.4	0.55		0.26	0.34	0.23	0.38
0.19	0.49	0.49	0.61	0.61	0.26	0.56	0.26	0.34	0.39	0.39	0.39	0.39	0.52	0.23	0.45	0.19	0.47	0.47	0.38	0.29	0.69	0.22	0.44	0.37	0.49	0.34	0.43	0.38	0.24
1.17	0.56	0.56	0.33	0.33	0.19	0.46	0.32	0.31	0.46	0.46	0.46	0.46	0.28	=	0.46	0.69	0.35	0.42	0.48	0.39	0.34	0.35	0.45	1.88	0.26	0.23	0.31	0.21	1.05
0.98	0.71	0.71	0.24	0.24	0.13	0.5	0.39	0.36	0.52	0.52	0.52	0.52	0.23	1.15	0.44	0.71	0.28	0.41	1.08	0.48	0.3	0.32	0.28	0.85	0.32	0.23	0.3	0.34	0.75
0.86	0.49	0.49	0.21	0.21	0.21	9.0	0.22	0.41	0.48	0.48	0.48	0.48	98.0	9.0	0.52	0.24	0.37	0.71	0.38	0.46	0.26	0.24	0.29	0.32	0.32	0.18	0.2	0.5	0.29
0.18	0.41	0.41	0.49	0.49	0.26	0.45	0.16	0.36	0.37	0.37	0.37	0.37	0.41	0.22	0.41	0.21	0.7	0.43	0.35	0.36	0.35	0.3	0.42	0.1	0.32	0.29	0.43	0.29	0.21
0.2	0.49	0.49	0.46	0.46	0.22	0.54	0.13	0.39	0.39	0.39	0.39	0.39	0.36	0.15	0.29	0.19	0.38	0.31	0.28	0.3	0.38	0.24	0.5	0.15	0.35	0.29	0.51	0.26	0.17
															-														
_	NFRSF6B v2	NFRSF6B v3	ILN1	RLN2 v1	XCR4	LC6A2	LRD1 v1	ICHL1	I TAC1 vB	AC1 vA	AC1 vC	AC1 v0	0XA2 v1	NXA13	PARA	DNF	(ST1	VSL5	PAP1	TBP2 v2	ICIAI	NXA7 v1	38H	.BI2	H28	HRNB4	DGFB	ALCYON	IRG1vSMDF
0.418333333 ESR	0.41 <i>7777778</i> TNFRSF6B	0.41777778 TNFRSF6B	0.416666667 RLN1	0.416666667 F	0.416111111 CXCR4	0.41444444 SLC6A2	0.412941176 KLRD1	0.411666667 UCH	0.41111111	0.41111111 TAC1	0.41111111 TAC1	0.41111111 TAC1	0.411111111 FOXA2 v	0.410555556 ANXA13	0.41 RARA	0.408888889 CDNF	0.406666667 MST	0.406111111 INSL5	0.40555556 SPAP1	0.40222222 CTBP2	0.401666667 SLC1A	0.4 ANXA7	0.4 SHBC	0.39944444 EBI2	0.398 THRB	0.39555556 CHRNB4	0.393888889 PDGFB	0.393529412 CALCYON	0.392352941 NRG1vSMDF
o.	0	0	0.	0	0.	0	0.	0.	0.	0.	0.	0.	0	0		0	0	0.	0	0.	0			0.		0.	0	0.	0.

FIG. 11-24B

0.15	0.31	0.31	0.36	0.36	0.35	0.15	0.37	0.42	0.42	0.42	0.42	0.42	0.35	0.28	0.36	0.26	0.31	0.4	0.35	0.47	0.37	0.69	0.33	0.13	0.37	0.26	0.4	0.76	
0.2	0.31	0.31	0.45	0.45	0.7	0.14	0.94	0.47	0.42	0.42	0.42	0.42	0.41	0.31	0.5	0.45	0.64	0.34	0.27	0.45	0.42	0.48	0.29	0.25	0.51	0.47	0.39	0.5	
0.19	0.27	0.27	0.41	0.41	2.66	0.19	0.53	0.42	0.36	0.36	0.36	0.36	0.43	0.4	0.34	0.37	0.42	0.34	0.21	0.45	0.55	0.77	9.0	0.12	0.33	0.32	0.46	0.67	1
0.4	0.32	0.32	0.38	0.38	9.0	0.23	1.25	0.37	0.32	0.32	0.32	0.32	0.5	0.52	0.5	0.42	0.32	0.33	0.32	0.43	0.51	0.52	0.61	0.17	0.69	1.76	0.71	0.57	9
0.19	0.24	0.24	0.62	0.62	0.29	0.23	0.47	0.55	0.49	0.49	0.49	0.49	0.45	0.33	0.31	0.4	0.27	0.28	0.35	0.56	0.5	0.73	0.49	0.33	0.5	0.42	0.38	0.47	3, 3
0.17	0.32	0.32	9.0	9.0	0.26	0.29	0.51	0.42	0.36	0.36	0.36	0.36	0.46	0.33	0.61	0.57	0.26	0.39	0.25	0.45	0.32	0.4	0.51	0.22	0.56	0.45	0.42	0.45	
0.61	0.53	0.53	0.32	0.32	0.25	0.74	0.21	0.5	0.46	0.46	0.46	0.46	0.39	0.33	0.35	0.62	0.24	0.47	0.41	0.38	0.27	0.7	0.29	0.51		0.5	0.34	0.19	0.00
0.26	0.36	0.36	0.44	0.44	0.3	0.36		0.34	0.35	0.35	0.35	0.35	0.34	0.3	0.4	0.34	0.72	0.43	0.52	0.44	0.55		- 0.33	0.24	0.28	0.32	0.52		000
0.3	0.42	0.42	0.29	0.29	0.26	0.5	0.53	0.4	0.34	0.34	0.34	0.34	0.36	0.4	0.54	0.3	9.0	0.34	0.75	0.36	0.43	0.36	0.35	0.36	0.32	0.55	0.3	0.36	110
0.26	0.33	0.33	0.46	0.46	0.28	0.31	0.15	0.46	0.39	0.39	0.39	0.39	0.31	0.2	0.38	0.17	0.48	0.32	0.41	0.33	0.39	0.42	0.26	0.31	0.35	0.27	0.29	0.25	000
0.58	0.44	0.44	0.41	.0.41	0.43	0.61	0.24	0.37	0.38	0.38	0.38	0.38	0.44	0.22	0.26	0.61	0.19	0.48	0.27	0.32	0.28	0.28	0.36	0.33	·	0.31	0.36	0.26	

FIG. 11-25A

		Ţ		_	Τ	_	,		_		1	_	T	Т	Τ	Г		Γ	Γ	Γ	Г							Γ-	
0.31	0.29	0.29	0.29		0.25	0.31	0.43	0.31	0.31			0.29	0.44	0.29	0.31	0.32	0.46	0.41	0.43	0.4	0.13	0.35		0.49	0.36	0.24	0.28	0.45	0.43
0.42	0.32	0.32	0.32	0.44	0.29	0.5	0.49	0.41	0.41	0.27	0.27	0.57	0.4	0.7	0.46	0.51	0.54	0.35	0.39	0.26	0.77	0.64	0.29	0.32		0.3	0.18	0.48	0.39
0.47	0.3	0.3	0.3	0.49	1.06	0.38	0.21	0.29	0.29	0.38	0.38	0.37	0.3	0.3	0.23	0.37	0.38	0.32	0.64	0.39	0.09	1.29	0.37	0.36	0.18	0.27	0.31	0.22	0.38
0.29	0.34	0.34	0.34	0.73	1.24	0.25	0.18	0.17	0.17	0.47	0.47	0.41	0.52	0.32	0.16	0.3	0.31	0.36	0.76	0.22	0.09	0.99	0.37	0.29	0.1	0.58	0.32	0.19	0.46
0.41	0.5	0.5	0.5	0.45	0.38	0.27	0.48	0.46	0.46	0.22	0.22	0.21	0.37	0.62	0.41	0.34	0.67	0.48	0.22	0.2	0.16	0.33	0.44	0.38	0.4	0.28	0.34	0.5	0.32
0.3	0.29	0.29	0.29	0.42	0.15	0.28	0.41	0.32	0.32	0.76	0.26	0.36	0.41	0.43	0.38	0.38	0.49	0.37	0.35	0.35	0.32	0.19	0.25	0.43	0.44	0.27	0.34	0.36	0.41
0.38	0.19	0.19	0.19	0.38	0.16	0.32	0.35	0.36	0.36	0.25	0.25	0.42	0.45	0.45	0.42	0.49	0.4	0.32	0.4	0.34	0.28	0.21	0.42	0.38	0.35	0.33	0.29	0.16	0.38
					W.						,																		
ICAM5	CASP7 va	- 1	CASP7 vD	NPPA	C4BPA	IFE3	GMFG	C4A	C4B		TNFSF11 v2	C48PB	NFK81	ITGA6	RPS5	CCL23 v1	EDN2	CXCL12	[5	CYP24	GRM8	<u> </u>	ADC-90	MMP9	F0XA1	RAMP2	RLN2 v2	GPR10	CCR3
19	=	=	0.391111111	0.385333333	0.383888889		0.383888889					0.382222222	_	0.381176471	0.380588235 RPS5	0.37944444		_	0.3777778	0.377222222 CYP24	h . ا	0.376666667	 l	0.371176471	0.370588235		0.37	0.368333333	0.36555556 CCR
	,																					اد	اد			٥			

FIG.11-25B

0.59	0.64	0.64	0.64	0.17	0.53	0.19	0.29			0.49	0.49	0.31	0.21	0.35	0.47	0.45	0.31	0.35	0.25	0.23	0.22	0.16	0.34	0.36	0.36	0.47	0.57	0.35	0.3
0.35	0.71	0.71	0.71	0.23	0.29	0.49	0.48	0.4	0.4			0.41	0.25	0.34	0.53	0.38	0.29	0.29	0.33	0.56	0.35	0.24	0.29	0.36	0.29	0.49	0.53	0.31	0.35
0.56	0.36	0.36	0.36	0.13	0.43	0.24	0.23	0.48	0.48	0.33	0.33	0.38	0.31	0.43	0.56	0.49	0.36	0.37	0.23	0.46	0.3	0.15	0.32	0.34	0.45	0.44		0.39	0.41
0.43	0.55	0.55	. 0.55	0.7	0.34	1.64	0.43	0.84	0.84	0.51	0.51	0.51	0.37	0.3	0.63	0.5	0.32	0.38	0.24	0.61	0.55	0.21	0.37		0,44	0.53	0.47	0.57	0.3
0.5	0.54	0.54	0.54	0.24	0.28	0.23	0.35	0.39	0.39	0.5	0.5	0.39	0.28	0.27	0.54	0.36	0.28	0.34	0.3	0.55	0.42	0.21		0.37	0.41	0.52	0.35	0.47	0.31
0.62	0.48	0.48	0.48	0.56	0.35	0.32	0.39	0.46	0.46	0.94	0.94	0.39	0.45			0.36	0.43	0.75	0.27	0.45	0.41	0.24	0.37	0.5	0.74	0.48	0.52	0.34	0.27
0.24	0.22	0.22	0.22		0.4	0.28	0.34	0.33	0.33			0.39	0.26	0.33	0.24	0.75	0.36	0.35	0.62	0.18	0.1	0.64		0.43	0.45	0.43	0.37	0.31	0.33
0.27	0.36	0.36	0.36	0.4	0.17	0.37	0.48	0.3	0.3	0.22	0.22	0.26	0.55	0.45	0.27	0.27	0.3	0.3	0.28	0.37	1.92	0.17	0.5	0.28	0.31	0.22	0.4	0.29	0.39
0.38	0.44	0.44	0.44	0.35	0.25	0.25	0.52	0.34	0.34	0.24	0.24	0.47	0.48	0.28	0.25	0.39	0.26	0.32	0.35	0.62	0.24	0.29	0.43	0.26	0.4	0.24	0.43	0.73	0.43
0.18	0.29	0.29	0.29	0.59	0.1	0.32	0.44	0.34	0.34	0.28	0.28	0.38	0.49	0.39	0.27	0.33	0.27	0.3	0.27	0.38	0.32	0.21	0.48	0.29	0.13	0.21	0.29	0.3	0.38
0.35	0.22	0.22	0.22		0.24	. 0.27	0.41	0.32	0.32			0.36	0.33	0.26	0.34	0.37	0.39	0.45	0.47	0.22	0.12	0.26		0.47	0.49		0.3	0.21	0.34

FIG. 11-26A

		_	_								_			_	_										_				
0.37	0.57	0.5	0.43	0.26	0.49	0.49		0.45		0.27	0.4	0.42	0.34	0.15	0.26	0.21	0.45	0.45	0.32	0.45	0.31	0.17	0.51	0.34	0.34	0.38	0.41	0.46	0.21
0.23	0.33	0.31	0.27	0.4	9.0	0.4	0.33	0.22	0.51	0.65	0.54	0.37	0.5	0.33	0.38	0.69	0.3	0.3	0.36	0.43	0.32	0.41	0.36	0.49	0.7	0.27	0.18	0.24	0.29
0.3	0.4	0.32	0.21	. 0.22	0.35	0.35	0.57	0.38	0.12	0.29	1.14	0.55	0.46	0.1	0.27	0.17	0.25	0.25	0.12	-	0.35	0.19	0.83	0.31	0.31	0.25	0.27	0.25	0.47
0.44	0.41	0.31	0.22	0.16	0.32	0.32	0.48	0.38	0.14	0.25	0.56	0.78	0.45	0.08	0.28	0.23	0.21	0.21	90.0	0.62	0.44	0.19	0.45	0.32	0.36	0.29	0.29	0.3	0.33
0.4	0.27	0.26	0.5	0.41	0.52	0.52	0.35	0.43	0.2	0.41	0.16	0.4	0.65	0.17	0.31	0.18	0.44	0.44	0.16	0.32	0.23	0.41	0.23	0.57	0.26	0.16	0.19	0.33	0.26
0.32	0.25	0.31	0.31	0.36	0.39	0.39	0.42	0.3	0.34	0.4	0.15	0.28	0.36	0.17	0.31	0.34	0.26	0.26	0.37	0.09	0.4	0.41	0.26	0.3	0.17	0.29	0.31	0.37	0.29
0.3	0.28	0.3	0.27	0.45	0.36	0.36	0.28	0.26	0.21	0.32	0.15	0.3	0.41	0.16	0.18	0.28	0.22	0.22	0.31	0.1	0.33	0.42	0.27	0.29		0.23	0.27	0.31	0.21
HTR7 vD	SRC	CD1B	TIMP1	SCN3A	PTPN6 v2	PTPN6 v3		CD28	HLA-DRB4	MDK	11.26	ADCYAP1	DUSP8	GAB1	RFX2 v2	IFNGR2	TRAF3 v1	TRAF3 v2	AVP .	CYP4A11	CCL11	PAPPA	OAT	RORB	KLK2	2002	MAZ	VIPR2	STAT3 v1
0.365	0.365	0.362352941	0.361764706	0.35944444	0.358333333	0.358333333	0.357333333	0.355555556	0.354666667	0.353529412	0.353333333	0.350555556	0.350555556	0.350555556	0.34944444	0.348333333	0.348333333	0.348333333	0.347222222	0.344705882	0.343888889	0.341764706	0.341666667	0.341111111	0.339411765	0.33875	0.336666667	0.336111111	0.335

0.42	0.34	0.49	0.51	0.26	0.18	0.18	0.31	0.29	0.4		0.15	0.25	0.23	0.48	0.42	0.21	0.26	0.26	0.39	0.16	0.43	0.36	0.19	0.24	0.32	0.33	0.39	0.45	0.37
0.42	0.5	0.34	0.35	0.31	0.33	0.33	0.31	0.36	0.36	0.39	0.31	0.5	0.19	1.35	0.35	0.38	0.48	0.48	0.28	0.29	0.34	0.36	0.37	0.23	0.47	0.54	0.3	0.36	0.46
0.48	0.39	0.71	0.41	0.26	0.16	0.16	0.34	0.42	0.29	0.35	0.16	0.2	0.2	0.7	0.38	0.46	0.31	0.31	0.4	0.26	0.28	0.45	0.21	0.35	0.48	0.48	0.45	0.38	0.37
0.38	0.59	0.58		0.29	99.0	99.0	0.26	0.46	0.53	0.43	0.18	0.21	0.2	0.5	0.47	0.65	0.72	0.72	0.35	0.5	0.36		0.2	0.3	0.64		0.53	0.34	0.42
0.36	0.38	0.41	0.33	0.3	0.18	0.18	0.39	0.33	0.63	0.35	0.43	0.33	0.2	0.53	0.33	0.41	0.35	0.35	0.33	0.35	0.33	0.54	0.18	0.3	0.45	0.58	0.52	0.42	0.44
0.61	0.36	0.39	0.35	0.3	0.27	0.27	0.4	0.52	0.85	0.47	0.33	0.3	0.29	0.35	0.28	0.45	0.58	0.58	0.69		0.52	0.38	0.35	0.35	0.39	0.45	0.4	0.31	0.33
0.35	0.36	0.16	0.64	0.3	0.39	0.39		0.29		0.25	0.65	0.51	0.37	0.18	0.56	0.17	0.45	0.45	0.25	0.52	0.45	0.22	0.41	0.41	0.23	0.27	0.32	0.27	0.24
0.29	0.22	0.45	0.35	0.65	0.42	0.42	0.3	0.32	0.26	0.27	0.29	0.17	0.35	0.37	0.24	0.37	0.16	0.16	0.5	0.2	0.22	0.38	0.37	0.37	0.31		0.27	0.26	0.24
0.34	0.22		0.31	0.56	0.36	0.36	0.32	0.32	0.29	0.37	0.31	0.22	0.37	0.3	0.31	0.5	0.26	0.26	0.31	0.25	0.32	0.4	0.35	0.31	0.39	0.4	0.37	0.38	0.54
0.26	0.26	0.4	0.31	0.41	0.36	0.36	0.3	0.35	0.19	0.35	0.23	0.35	0.38	0.27	0.35	0.29	0.15	0.15	0.55	0.15	0.23	0.33	0.33	0.34	0.22	0.25	0.3	0.32	0.34
0.3	0.44	0.22	0.38	0.57	0.31	0.31	·	0.35		0.19	0.22	0.47	0.36	0.12	0.61	0.31	0.42	0.42	0.5	0.2	0.33	0.19	0.28	0.32	0.23	0.25	0.29	0.33	0.22

	T-	T -	_	·		,		_			_	1			1				i	[_				
0.21	0.4	0.4	0.4	0.32	0.15	0.15	0.17	0.26	0.42	0.25	0.16	0.28	0.5	0.24	0.25	0.28	0.26	0.28	0.3	0.28	0.23	0.19	0.21	0.32	0.25	0.28	0.19	0.3	0.25	0.17
0.29	0.27	0.27	0.27	0.49	0.47	0.47	0.74	0.47	0.41	0.32	0.99	0.36	0.2	0.27	0.22	0.32	0.64	0.42	0.35	0.56	0.36	0.17	0.3	0.47	0.59	0.37	0.45	0.33	0.23	0.22
0.47	0.32	0.32	0.32	0.21	0.25	0.25	0.13	0.24	0.72	0.18	0.09	0.17	0.61	0,16	0.28	0.42	0.21	0.55	0.5	0.3	0.09	0.5	0.17	0.35	0.28	0.21	0.11	0.26	0.53	0.34
0.33	0.38	0.38	0.38	0.25	0.32	0.32	0.11	0.37	0.48	0.21		0.17	96.0	0.15	0.17	0.48	0.21	0.21	0.7	0.27	0.07	0.21	0.17	0.5	0.28	0.26	0.15	0.32	0.38	0.48
0.26	0.23	0.23	0.23	0.37	0.29	0.29	0.27	0.55	0.54	0.22	0.28	0.3	0.38	0.56	0.38	0.47	0.23	0.16	0.37	0.25	0.21	99.0	0.32	0.49	0.29	0.44	0.38	0.27	0.18	0.23
0.29	0.26	0.26	0.26	0.37	0.4	0.4	0.57	0.33	0.37	0.36	0.48	0.36	0.17	0.39	0.35	0.3	0.49	0.5	0.32	0.34	0.37	0.31	0.32	0.31	0.32	0.37	0.35	0.22	0.17	0.25
0.21	0.25	0.25	0.25	0.4	0.36	0.36	0.47	0.34	0.42	0.35	0.72	0.38	0.18	0.33 (0.29	0.29	0.28	0.21	0.28	0.31	0.21	0.26	0.29	0.31	0.23	0.35	0.35	0.32	0.23	0.27
0.335 STAT3 v2	0.33388889 PTPN7 v1	0.33388889 PTPN7 v2		0.333529412 G1P2	0.33222222 CDK4 v1	0.332222222 CDK4 v2	0.33055556 DPP4		0.32833333 LEP	0.32777778 SPP1		0.327222222 NPPC	0.327222222 CYSLTR2	0.325882353 GRID2	0.323888889 CXCR6	$\overline{}$	0.32055556 PRDM1		-		0.317222222 [PTGIS		0.31 IFRD2	0.30944444 SERPINE1		0.307058824 CCKAR	0.30555556 MAFF	0.305 TRHR	0.30222222 TNFSF13B	0.29944444 SELPLG

FIG.11-27B

0.37	0.24	0.24	0.24	0.23	0.36	0.36	0.13	0.31	0.08	0.27	0.15	0.36	0.22	0.4	0.32	0.23	0.28	0.21	0.49	0.18	0.55	0.44	0.42	0.15	0.2	0.21	0.22	0.33	0.32	0.34
0.46	0.36	0.36	0.36	0.76	0.35	0.35	0.22	0.26	0.15	0.35	0.19	0.32	0.17	0.4	0.38	0.26	0.34	0.4	0.32	0.19	0.24	0.33	0.27	0.17	0.46		0.4	0.39	0.37	0.32
0.37	0.3	0.3	0.3	0.3	0.3	0.3	0.14	0.34	0.1	0.22	0.11	0.31	0.27	0.35	0.33	0.22	0.22	0.26	0.48	0.21	0:39	0.3	0.54	0.2	0.28	0.19	0.36	0.42	0.37	0.33
0.42	0.31	0.31	0.31	0.44	0.38	0.38	0.18	0.31	0.18	0.53	0.12	0.32	0.22	0.33	0.43	0.23	0.3	0.52	0.48	0.41	0.5	0.42	0.56	0.2	0.38	0.36	0.3	0.31	0.36	0.34
0.44	0.32	0.32	0.32		0.34	0.34	0.22	0.3	0.13	0.31	0.16	0.36	0.19	0.37	0.44	0.21	0.29	0.37	0.46	0.15	0.39	0.48	0.3	0.15	0.35	0.26	0.49	0.38	0.42	0.29
0.33	0.38	0.38	0.38	0.29	0.33	0.33	0.45	0.37	0.17	0.29	0.2	0.59	0.24	0.46	0.36	0.69	0.22	0.4	0.36	0.85	0.69	0.4	0.56	0.21	0.34	0.45	0.35	0.33	0.47	0.38
0.24	0.35	0.35	0.35	0.34	0.15	0.15	0.14	0.27	0.52	0.95	0.07	0.27	0.52	0.21	0.19	0.33	0.31	0.31	0.21	0.24	0.22	0.21	0.22	0.38	0.28	0.21	0.24	0.27	0.25	0.2
0.24	0.49	0.49	0.49	0.36	0.46	0.46	0.46	0.33	0.29	0.23	0.73	0.25	0.18		0.46	0.24	0.46		0.23	0.35	0.21	0.24	0.27	0.34	0.23	0.39	0.32	0.25	0.15	0.32
0.54	0.36	0.36	0.36	0.31	0.52	0.52	0.31	0.26	0.35	0.5	0.33	0.37	0.25	0.32	0.41	0.25	0.47	0.45	0.23	0.29	0.23	0.35	0.25	0.4	0.28	0.34	0.35	0.23	0.29	0.45
0.34	0.26	0.26	0.26	0.29	0.42	0.42	0.59	0.32	0.27	0.38	.0.68	0.39	0.18	0.32	0.4	0.25	0.35	0.27	0.19	0.3	0.27	0.25	0.7	0.55	0.52	0.27	0.5	0.25	0.14	0.32
0.22	0.53	0.53	0.53	0.44	0.13	0.13	0.65	0.32	0.31	0.28	0.11	0.55	0.45	0.28	0.17	0.31	0.21	0.21	0.26	0.23	0.48	0.22	0.21	0.29	0.21	0.26	0.19	0.31	0.3	0.10

FIG.11-28A

FIG.11-28B

0.35	0.0	0.14	0.75	0.46	0.27	0.36	0.44	0.25	0.15	0.2	0.75	0.4	0.4	0.0	0.31	0.2	0.15	0.14	0.24	0.45	0.18	0.31	0.31	0.37	0.19	0.25	0.53	0.26
0.38	0.2	0.24	0.51	0.38	0.21	0.43	0.32	0.37	0.25	0.17	0.32	0.23	0.23	0.3	0.46	0.3	0.32	0.16	0.32	0.29	0.24	0.37	0.33	0.28	0.23	0.19	0.58	0.48
0.31	0.16	0.14	0.65	0.37	0.33	0.31	0.99	0.3	0.21	0.23	0.46	0.23	0.23	0.3	0.58	0.21	0.29	0.16	0.26	0.37	0.21	0.34	0.34	0.29	0.16	0.21	0.51	0.24
0.33	0.18	0.32	0.53	0.41	0.26	0.39	69.0	0.69	0.25	0.5	0.93	0.33	0.33	0.27	0.5	0.62	0.27	0.22	0.28	0.38	0.38	0.34	0.34	0.33	0.29	0.26	0.74	0.31
0.35	0.23	0.24	0.54	0.43	0.24	0.56	0.4	0.31	0.21	0.19	0.25	0.26	0.26	0.21	0.28	0.27	0.32	0.16	0.26	0.28	0.18	0.35	0.31	0.34	0.21	0.28	0.48	0.27
	0.14	0.36	0.51	0.5	0.24	0.35	0.45	0.36	0.18	0.27	0.36	0.29	0.29	0.34	0.58	0.19	0.35	0.39	0.31	0.58	0.23	0.41	0.53	0.35	0.28	0.39	0.58	0.27
0.28	0.35	0.29	0.15	0.19	0.37	0.15	0.1	0.22	0.31	0.2	0.21	0.36	0.36	0.47	0.15	0.31		0.27	0.21	0.16	0.49		0.15		0.25	0.26	0.09	0.21
0.22	0.42	0.22	0.07	0.18	0.27	0.3	0.13	0.17	0.27	0.35	0.16	0.27	0.27	0.28	0.5	0.18	0.28	0.23	0.32	0.29	0.17	0.15	0.23	0.37	0.24	0.22	0.14	0.23
0.27	0.41	0.28	0.13	0.21	0.24	0.34	0.2	0.23	0.21	0.22	0.24	0.27	0.27	0.22	0.21	0.24	0.29	0.22	0.4	0.32	0.19	0.15	0.2	0.25	0.36	0.21	0.21	0.47
0.18	0.28	0.19	0.17	0.21	0.22	0.39	0.12	0.2	0.36	0.45	0.13	0.21	0.21	0.2	0.1	0.16	0.28	0.2	0.21	0.3	0.15	0.15	0.12	0.23	0.22	0.21	0.15	0.2
0.42	0.24	0.36	0.15	0.2	0.24	0.17	0.12	0.2	0.45	0.21	0.28	0.29	0.29	0.39	0.2	0.24		0.22	0.19	0.12	3.5	!	0.18		0.18	0.29	0.12	0.14

FIG.11-29A

	Π	Π	Τ	T	Т	T		_	T	_	Τ																		γ
0.24	0.19	0.32		0.23	0.28	0.24	0.26	0.26	0.21	0.26	0.29	0.22	0.29	0.21	0.37	0.27	0.2	0.5	0.19	0.32	0.33	0.16	0.16	0.22	0.19	0.19	0.19	0.19	0.39
0.22	0.32	0.35	0.3	0.22	0.24	0.37	0.27	0.27	0.33	0.29	0.33	0.24	0.26	0.25	0.24	0.32	0.44	0.2	0.25	0.19	0.32	0.28	0.28	0.2	0.22	0.22	0.22	0.22	0.45
0.34	0.16	0.27	0.18	0.5	0.78	0.5	0.19	0.19	0.16	0.14	0.25	0.25	0.24	0.17	0.57	0.29	0.12	0.27	0.24	0.27	0.53	0.09	0.09	0.15	0.11	0.11	0.11	0.11	0.25
0.55	0.18	0.47	0.2	0.63	0.64	0.52	0.2	0.7	0.12	0.14	0.21	0.3	0.34	0.18	0.56	0.26	0.1	0.41	0.19	0.39	0.31	0.1	0.1	0.18	0.11	0.11	0.11	0.11	0.28
0.24	0.33	0.24	0.23	0.21	0.8	0.19	0.32	0.32	0.18	0.24	0.25	0.24	0.34	0.31	0.36	0.31	0.15	0.34	0.33	0.33	0.14	0.16	0.16	0.21	0.26	0.26	0.26	0.26	9.0
0.2	0.3	0.22	0.21	0.19	0.1	0.24	0.3	0.3	0.3	0.2	0.26	0.25	0.31	0.24	0.19	0.27	0.39	0.27	0.22	0.18	0.19	0.25	. 0.25	0.2	0.23	0.23	0.23	0.23	0.48
0.13	0.25	0.26		0.15	0.08	0.26	0.31	0.31	0.32	0.24	0.33	0.24	0.3	0.24	0.22	0.3	0.47	0.27	0.21	0.2	0.25	0.22	0.22	0.24	0.16	0.16	0.16	0.16	0.28
1 1	[_	$\neg \neg$		- 1		WISP1					\neg							235294 TGFB3		-		-		TRPV				11111 PPBP
0.277	0.2776	0.2761	0.2757	0.2755		0.2738	0.2738	0.2738	0.2738	0.2727	0.271111111	0.270555556			0.26944444	0.268333333	0.268333333	0.268235294	0.268235294	0	0.26777778	0.26722222	0.26722222	0.267058824	0.26666667	0.26666667	0.26666666	0.266666667	0.26611111

0.26	0.26	0.16	0.21	0.22	0.14	0.16	0.25	0.25	0.31	0.24	0.21	0.31	0.28	0.27	0.16	0.2	0.22	0.26		0.31	0.17	0.23	0.23	0.36	0.41	0.41	0.41	0.41	0.11
0.48	0.46	0.19	0.29	0.26	0.24	0.22	0.29	0.29	0.37	0.43	0.23	0.37	0.25	0.63	0.2	0.23	0.21		0.54	0.33	0.24	0.37	0.37	0.37	0.4	0.4	0.4	0.4	0.1
0.24	0.31	0.14	0.23	0.24	0.16	0.15	0.19	0.19	0.31	0.26	0.32	0.26	0.19	0.25	0.2	0.39	0.28	0.23	0.26		0.23	0.37	0.37	0.33	0.37	0.37	0.37	0.37	-0.15
0.31		0.21	0.36	0.33	0.13	0.22	0.3	0.3	0.28	0.41	0.32	0.43	0.26	0.39	0.22	0.29	0.31	0.32	0.29		0.24	0.7	0.7	0.37	0.39	0.39	0.39	0.39	0.32
0.27	0.37	0.41	0.31	0.29	0.13	0.25	0.27	0.27	0.26	0.35	0.23	0.23	0.21	0.33	0.2	0.21	0.19	0.24	0.42	0.37	0.21	0.45	0.45	0.41	0.36	0.36	0.36	0.36	0.12
0.27	0.4	0.18	0.5	0.31	0.21	0.24	0.41	0.41	0.34	0.2	0.32	0.5		0.28	0.19	0.3	0.26	0.28	0.5	0.26	0.22	0.43	0.43	,	0.64	0.64	0.64	0.64	0.24
0.21	0.7	0.52		0.28	0.47	0.33	0.24	0.24	0.5	0.29	0.28	0.23	0.23	0.21	0.34	0.25	0.12	0.21	0.12	0.18	0.37	0.09	0.09	0.25	0.17	0.17	0.17	0.17	0.3
0.23	0.29	0.18	0.27	0.24	0.18	0.25	0.29	0.29	0.38	0.33	0.21	0.22	0.21	0.17	0.15	0.23	0.44	0.3	0.27	0.24	0.31	0.2	0.2	0.16	0.17	0.17	0.17	0.17	0.14
0.47	0.28	0.24	0.32	0.33	0.15	0.25	0.29	0.29	0.39	0.29	0.19	0.19	0.27	0.24	0.21	0.7	0.46	0.33	0.15	0.24	0.32	0.35	0.35	0.19	0.21	0.21	0.21	0.21	0.16
0.2	0.21	0.31	0.25	0.15	0.11	0.22	0.26	0.26	0.32	0.32	0.23	0.17	0.31	0.2	0.14	0.22	0.33	0.25	0.23	0.21	0.24	0.7	0.2	0.37	0.16	0.16	0.16	0.16	0.21
0.14	0.21	0.3	·	0.18	0.11	0.32	0.29	0.29	0.15	0.28	0.42	0.22	0.3	0.29	0.33	0.29	0.14	0.18	0.15	0.27	0.2	0.16	0.16	0.33	0.24	0.24	0.24	0.24	0.21

0.70	0.38	0.13	0.52	0.00	0.24	0.21	0.20	0.39	0.39	0.32	0.34	0.13	0.13	0.21	0.13	9,0	0.15	0.41	0.19	0.29	0.44	0.21	0.18	0.18	0.26	0.27		0.22	0.16
, 00	0.2	76.0	0.25	0.24	0.28	0.28	0.24	0.36	0.2	0.28	0.16	0.63	0.59	0.39	0.18	0.18	0.41	0.33		0.17	0.18	0.22	0.63	0.22	0.27	0.54	0.26	0.3	0.25
0.50	0.30	0.18	0.22		0.22	0.3	0.11	0.55	0.35	0.23	0.42	0.09	0.12	0.24	0.12	0.28	0.16	0.68	0.27	0.33	0.37	0.16	0.26	0.15	0.75	0.27	. 0.09	0.26	0.14
30.0	0.20	0.31	0.76	0.07	0.21	0.43	0.11	0.3	0.43	0.2	0.36	0.11	0.13	0.19	0.1	0.36	0.19	0.22	0.19	0.48	0.23	0.18	0.1	0.15	0.51	0.22	0.1	0.2	0.12
0.18	0.33	0.11	0.28	0.17	0.16	0.4	0.16	0.13	0.14	0.25	1.55	0.22	0.36	0.46	0.12	0.43	0.38	0.18	0.27	1.32	0.19	0.18	0.4	0.15	0.28	0.25	0.2	0.21	0.2
000	0.15	0.2	0.3	0.15	0.21	0.18	0.22	90.0	0.17	0.35	0.09	0.38	0.41	0.27	0.12	0.19	0.25	0.13	0.31	0.1	0.17	0.15	0.38	0.14	0.15	0.29	0.13	0.33	0.18
0.07	0.11	0.16	0.25	0.08	0.22	0.17	0.25	0.09	0.18	0.31	0.11	0.28	0.33	0.28	0.11	0.17	0.25	0.16	0.23	0.12	0.17	0.13	0.35	0.13	0.08	0.24	0.25	0.33	0.18
MASP1 v2	CYP17	MGST2	CD5	NAALAD2	MYD88	CHRNG	L5RA	F	lL6	盂	BDNF	PMX2B	PTPN22 v1	SAMHD1	CHRNA3	NR0B1	ATM v1	- 1	ANXA7 v2	HTR1F	LHX3	SIAI5B	NCOA1 v1	CABRA3	SLC25A20	ALDH8A1	INFRSF138	PGRMC2	PCSKZ
0.265882353	0.26444444		~				=	-								5			0.25 ₽	0.25				_			-		0.245555556 P
0	0	0	0	0	·	0	Ö		0	0	0	0	0	Ö	o 		0	0				0.0	o l	0	:	0.7	0.7	0.7	0.7

FIG.11-30A

2,0	0.13	0.24	ري دي	0.22	0.4	0.32	0.2	0.43	0.0	0.02	0.10	200	0.25	0.19	0.24	0.27	0.57	0.10	27.0	0.00	0.20	0.15	0.73	0 13	0.12	0.11		- 00	0.23	0.33
700	0.24	72.0	0.30	0.25	9.0	0.31	0.24	0.3	0.3	0.15	0.16	5	0.19	0.13	0.22	0.64	0.18	0.70	0.0	0.15	0.10	0.10	0.39	0 11	0.35	0.00	10 0	2.0	0 18	0.34
		0.4	07.0	0.0	0.25	0.46	0.28	0.24	0.15	0.19	0.19	0.12	0.2	0.16	0.27	0.43	0.3	0.44	0.1	0.1	0.12	0.17	0.29	0.12	0.36	0 18	0.10	0.76	0.20	0.33
660	77.0	00.00	0.40	0.33	0.0	0.34	0.18	0.54		.0.55	0.22	0.2	0.35		0.3	0.84		0.78	0.09	0.23	0.19	0.4	0.85	0.16	0.78	0.14	020	0.50	0.23	0.55
0.21	0.31	0.2	10 O	72.0	0.37	0.46	0.21	0.36	0.33	0.28	0.15	0.11	0.25	0.14	0.19	0.46		0.23	0.15	0.23	0.14	0.18	0.34	0.12	0.37	0.11	0.22	0.38	0.22	0.31
0.23	0.40	0.42	0.50	0.02	0.07	0.75	0.26	0.45		0.27	0.23	0.17	0.27	0.29	0.37	0.44	0.38	0.23	0.24	0.43	0.14	0.21	0.33	0.22	0.38			0.79	0.44	0.3
0.46	0.18	0.71	0.23	0.08	0.00	0.17	0.38	0.17	0.28	0.28	0.33	0.27	0.21	0.15	0.21	0.12	0.25	0.19	0.38	0.15	0.33	0.41	0.17	0.2	0.15	0.41	0.17		0.24	0.13
0.13	0.18	0.19	0.39	0.21	17.0	47.0	7.0	0.22	0.27	0.17	0.27	0.06	0.26	0.35	0.18	0.14	0.22		0.21	0.36	0.13	0.14	0.21	0.31			0.3	0.12	0.18	0.27
0.17	0.3	0.29	0.24	0.26	0.23	0.23	0.24	0.77	0.33	0.2	0.3	0.13	0.3	0.24	0.24	0.14	0.26	0.19	0.24	0.3	0.15	0.19	0.22	0.22	0.22	0.19	0.22	0.12	0.21	0.25
0.14	0.15	0.17	0.25	0.08	0.24	0.00	77.0	0.22	0.31	0.17	0.29	0.11	0.51	0.38	0.12	0.08	0.16	0.25	0.27	0.32	0.11	0.13	0.1	0.36	0.11	0.13	0.2	0.13	0.22	0.23
0.13	0.17	0.13	0.22	90.0	0 16	0.20	10.0	0.0	0.1	0.51	0.3	17:0	0.19	0.73	0.17	83.0	0.24	0.22	0.44	0.14	0.23	0.58	0.22	17.7	0.17	0.25	0.7		0.28	0.13

	T	T	T	Т	Т	T	T	Т	,	Τ	Τ	Τ	Τ	Τ	Τ	T	Τ	T	T	\top	Τ	T-		-	T	T	_	_	
0.4	0.31	76.0	0.16	0.18	0.78	0.0	0.76	0.78	0.17	0.38	0.19	0.55	0.17	0.17	0.17	0.17	0.17	0.11	0.15	0.51	0.16	0.22	0.22	0.85	0.16	0.16	0.17	0.19	0.18
0.29	0.23	0.39	0.18		0.16	0.22	0.31	0.43	0.31	0.27	0.22	0.24	0.27	0.27	0.27	0.27	0.27	0.49	0.23	0.3	0.23	0.19	0.19	0.18	0.19	0.32		0.25	0.36
0.56	0.44	0.16	0.14	0.14	0.24	0.13	0.16	0.2	0.17	0.46	0.15	0.46	0.15	0.15	0.15	0.15	0.15	90.0	0.17	0.21	0.12	0.73	0.73	0.09	0.21	0.23	0.14	0.11	0.19
0.25	0.5	0.15	0.13	0.16	0.2	0.11	0.15	0.16	0.16	0.2	0.15	0.24	0.12	0.12	0.12	0.12	0.12	0.04	0.19	0.23	0.11	0.43	0.43	0.56	0.2	0.28	0.15	0.11	0.19
0.16	0.46	0.2	0.25	0.16	0.34	0.21	0.36	0.46	0.25	0.17	0.18	0.65	0.36	0.36	0.36	0.36	0.36	0.16	0.19	0.22	0.14	0.47	0.47	0.14	0.2	0.24	0.26	0.23	0.32
0.15	0.13	0.46	0.13	0.16	0.27	0.25	0.36	0.29	0.31	0.16	0.23	0.13	0.25	0.25	0.25	0.25	0.25	0.31	0.15	0.18	0.19	0.7	0.1	0.2	0.11	0.32	0.15	0.19	0.24
0.16	0.14	0.19	0.11	0.13	0.28	0.21	0.37	0.23	0.19	0.16	0.2	0.12	0.28	0.28	0.28	0.28	0.28	0.28	0.14	0.16	0.17	0.1	0.1	0.13	0.18	0.29	0.11	0.12	0.18
		-																											
WMP2	CGA	₽	CHRNA2	283	1.24	NELL2	RFXANK v1	CCRL2	EGR1	CF IR	1.178	IRF5 v1				— I.	ASP1 VE	SES	TIMM23		CEBPG		WISP3 VZ	CCL26	HLA-DPA1	ADORA1	1MP.25	FCGRIA	SMK
	0.244705882		0.24444444	_	1			0.24222222	1.	_	0.241111111	0.241111111	0.24 CASP1	0.24 CASP1	0.24 (0.24 CASP1	0.24 CASP					_	- 1	0.235882353		0.234/05882 A		0.23411/64/ 1	U.233229412 USMK
Ö	Ö	O	0	ľ	o	o o	<u>ن</u>	<u>ن</u>	o) (-j c	-j c	Ö							0	o o	0	Ö	o o	0.7	0	0.7	6	7.0	0.7

FIG.11-31A

0.12	0.12	0.15	0.27	0.24	0.22	0.32	0.12	0.12	0.25	0.00	0.27	90.0	0.32	0.32	0.32	0.32	0.32	0.26	0.17	0.15	0.24	0.11	0.11	0.19	0.32	0.09	0.29	0.25	0.24
0.18	0.17	0.22	0.45	0.41	0.26	0.59	0.15	0.1	0.25	0.16	0.29	0.09	0.22	0.22	0.22	0.22	0.22	0.17	0.25	0.17	0.24	0.15	0.15			0.15	0.35	0.33	0.5
0.1	0.16	0.22	0.45	0.32	0.26	0.31	0.14	0.18	0.29	0.16	0.23	70.0	0.26	0.26	0.26	0.26	0.26	0.23	0.22	0.16	0.27	0.12	0.12	0.5	0.37	0.22	0.38	0.36	0.37
0.22		0.47	0.47	0.58	0.21	0.28	0.16	0.19		0.19	0.32	0.09					,	0.21	0.39	0.19	0.48	0.16	0.16	0.16	0.36				
0.19	0.19	0.23	0.39	0.38	0.3	0.33	0.15	0.11	0.28	0.5	0.39	0.07	0.27	0.27	0.27	0.27	0.27	0.17	0.28	0.19	0.38	0.21	0.21	0.25	0.31	0.15	0.47	0.44	0.29
0.22	0.24	0.22	0.61	0.36	0.23	0.25	0.17	0.21	0.35	0.3	0.5	0.19	0.46	0.46	0.46	0.46	0.46	0.46	0.3	0.18	0.36	0.37	0.37	0.27	0.44	0.5	0.37	0.42	0.34
0.38	0.31	0.16	0.11	0.1	0.29	0.16	0.3	0.27	0.27	0.3	0.24	0.44	0.21	0.21	0.21	0.21	0.21	0.08	0.15	0.3	0.14	0.28	0.28	0.14	0.18	0.1	0.12	0.15	0.11
0.24	0.14	0.31	0.15		0.23	0.19	0.26	0.35	0.14	0.28	0.16	0.16	0.2	0.2	0.5	0.2	0.5	0.47	0.83	0.21	0.45	0.1	0.1	0.15	0.21	0.39	0.15	0.18	0.25
0.23	0.16	0.26	0.16	0.32	0.22	0.23	0.27	0.32	0.32	0.34	0.19	0.14	0.18	0.18	0.18	0.18	0.18	0.43	0.2	0.27	0.26	0.21	0.21	0.15	0.11	0.42	0.37	0.33	0.19
0.28	0.11	0.21	0.12	0.13	0.2	0.22	0.37	0.18	0.26	0.33	0.21	0.17	0.18	0.18	0.18	0.18	0.18	0.23	0.15	0.27	0.16	0.14	0.14	0.15	0.21	0.31	0.13	0.14	0.18
0.29	0.35	0.2	0.12	0.14	0.2	0.15	0.3	.0.28	0.14	0.5	0.22	0.47	0.18	0.18	0.18	0.18	0.18	0.16	0.15	0.4	0.18	0.18	0.18	0.2	0.24	0.12	0.14	0.18	0.14

FIG.11-31B

0.0	0.17	0.12	0.42	0.42	0.08	0.22	0.15	1.5	0.14	0.07	0.2	0.24	0.08	0.18	0.22	0.22	0.22	0.29	0.24	0.15	0.19	0.23	0.23	0.23	0.17	0.17	0.26	0.26
0.3	0.24	0.34	0.26	0.26	0.13	0.23	0.42	0.18		0.17	0.26	.0.26	0.24	0.29	0.23	0.27	0.28	0.24	0.34		0.27	0.27	0.27	0.27	0.19	0.3	0.31	0.31
0.78	0.24	0.14	0.14	0.14	0.03	0.3	0.12	0.07	90:0	0.04	0.2	0.25	90:0	0.22	0.4	0.61	0.21	0.2	0.11	0.31	0.07	0.09	0.09	0.09	0.14	0.12	0.2	0.2
0.39	0.3	0.11	0.1	0.1	0.04	0.36	0.14	0.05	0.11	0.03	0.2	0.17	0.04	0.21	0.19	0.13	0.13	0.26	0.16	0.22	0.05	0.08	0.08	0.08	0.24	0.16	0.13	0.13
0.46	0.27	0.22	0.31	0.31	6).0	0.35	0.35	0.19	0.16	0.1	0.29	0.15	0.14	0.26		0.19	0.23	0.18	0.26	0.37	0.16	0.26	0.26	0.26	0.32	0.51	0.33	0.33
0.18	0.14	0.18	0.25	0.25	0.00	0.18	0.08	0.1	0.12	0.13	0.26	0.13	0.15	0.22	0.19	0.21	0.17	0.23	0.11	0.27	0.25	0.32	0.32	0.32	0.12	0.23	0.23	0.23
0.21	0.13	0.15	0.22	0.22	0.05	0.15	0.09	0.08	0.18	0.11	0.19	0.13	0.1	0.23	0.15	0.22	0.21	0.5	0.1	0.5	0.25	0.25	0.25	0.75	0.1	0.19	0.15	0.15
S100A12	SLAM	FADD	CYP11B1	CYP11B2	HSD3B1	NR2C1	TLR:1	EN2	PER3	INFRSF18 v1	·			NTRK2	1.155	TRPM2	CROT	MBL2	RGN v1	ICSBP1	IFNAR2	PTPRC v1	PTPRC v2	PTPRC v3	TIAF1 v1	FLT3	CASP3 va	CASP3 vb
0.233333333	0.233333333	0.233333333	0.233125	0.233125		0.23277778	0.23222222	0.23222222	0.231764706	0.231666667	0.230588235	0.230588235	0.23	0.229411765	0.228823529	0.228333333		3	\neg	0.225882353	0.22555556	0.225	0.225	_				0.224117647

FIG.11-32A

yes

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正

0.17	0.21	0.39	0.17	0.17	0.28	0.17	0.5	0.18	0.19	0.48	0.23	0.17	0.44	0.24	0.25	0.23	0.19	0.31	0.17	0.18	0.29	0.15	0.15	0.15	0.42	0.25	0.16	0.16	0.17
0.23	0.29	0.36	0.17	0.17	0.28	0.26	0.43	0.19	0.38	0.42	0.7	0.33	0.61	0.21	0.33	0.34	0.28	0.19	0.75	0.18	0.32	0.18	0.18	0.18	0.38	0.19	0.18	0.18	0.2
0.25	0.3	0.44	0.16	0.16	0.48	0.16	0.19	0.17	0.3	0.39	0.18	0.28	0.47	0.27	0.14	0.12	0.25	0.15	0.28	0.19	0.26	0.18	0.18	0.18	0.46	0.22	0.19	0.19	0.25
0.23	0.42	0.32	0.25	0.25	0.5	0.28	0.3	0.32	0.86	0.8	0.27	0.28	0.41		0.24	0.07	0.45		0.62	0.24	. 0.3	0.3	0.3	0.3	0.32	0.26			0.48
0.21	0.25	0.22	0.17	0.17	0.34	0.22	0.28	0.19	0.41	0.54	0.28	0.3	0.51	0.22	0.26	0.27	0.24	0.37	0.3	0.24	0.25	0.27	0.27	0.27	0.22	0.18	0.25	0.25	0.2
0.3	0.34	0.44			1.36	0.22	0.55	0.27	0.37	0.28	0.26	0.25	0.32	0.28	0.23	0.19	0.42		0.34	0.3	0.41	0.54	0.54	0.54	0.43	0.44	0.34	0.34	0.32
0.2	0.17	0.09	0.28	0.28	0.05	0.25	0.23	0.08	0.08	0.04	-	0.18	0.07	0.18	0.28	90.0	0.22	0.21	0.16	0.22	0.09	0.23	0.23	0.23	0.15	0.17	0.2	0.5	0.16
0.14	0.18	0.16				0.22	0.15	0.1	0.15	0.22	0.27	0.29	0.16	0.3	0.18	0.31	0.13	0.17	0.1	0.19	0.35	0.11	0.11	0.11	0.09	0.7	0.2	0.2	0.22
0.19	0.23	0.22	0.24	0.24	90.0	0.19	0.26	0.21	0.2	0.15	0.27		0.16	0.23	0.3	0.31	0.15	0.21	0.21	0.19	0.29	0.15	0.15	0.15	0.1	0.18	0.3	0.3	0.24
0.1	0.15	0.19	0.19	0.19	0.04	0.18	0.13	0.05	0.11	0.12	0.21	0.33	0.1	0.19	0.15	0.24	0.1	0.18	0.1	0.21	0.15	0.12	0.12	0.12	0.07	0.11	0.5	0.5	
0.23	0.17	0.11	0.4	0.4	0.09	. 0.25	0.11	0.75	0.12	0.08	0.15	0.18	.0.08	0.17	0.15	0.12	0.22	0.25	0.22	0.18	0.11	0.32	0.32	0.32	0.13	0.16	0.18	0.18	0.12

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0.27	0.29	0.23	0.2			0.16	0.13	0.15	0.22		0.14	0.16	0.12	0.11	0.19	0.27	0.23	0.23	0.17	0.18	0.14		0.28	0.07	0.21	0.17	0.15	0.24	0.19
0.44	0.18	0.24	0.2	0.17	0.47	0.3	0.58	0.27		0.31	0.24	0.24	0.22	0.19	0.34	0.55	0.24	0.24	0.22	0.31	0.21	0.19	0.26	0.18	0.18		0.18	0.35	0.33
0.13	0.26	0.18	0.19	0.47	0.05	0.13	0.07	0.08	0.07	0.08	0.17	0.22	0.12	0.22	0.13	0.11	0.24	0.24	0.1	0.26	0.22	0.11	0.18	0.04	0.22	0.12	0.27	0.25	0.12
0.11	0.22	0.14	0.12	0.39	0.05	0.11	0.08	0.06	0.06	0.12	0.12	0.16	0:08	0.28	0.13	0.1	0.27	0.27	0.07	0.19	0.12	0.1	0.15	0.04	0.24	0.13	0.17	0.27	0.1
0.11	0.16	0.8	0.17	0.21	0.09	0.33	0.21	0.14	0.1	0.12	0.15	0.75	0.19	0.22	0.21	0.33	0.24	0.24	0.28	0.18	0.17	0.26	0.27	0.11	0.28	0.28	0.2	0.32	0.16
0.34	0.15	0.17	0.13	0.14	0.43	0.21	0.31	0.23	0.15	0.24	0.17	0.7	0.24	0.26	0.19	0.26	0.19	0.19	0.19	0.2	0.13	0.24	0.18	0.08	0.14	0.62	0.14	0.16	0.28
0.29	0.15	0.13	0.13	0.14	0.46	0.16	0.31	0.26	0.2	0.3	0.18	0.22	0.27	0.13	0.18	0.28	0.16	0.16	0.17	0.2	0.17	0.23	0.17	0.08	0.13	0.19	0.12	0.15	0.29
SCN1A	MICA	L18R1	ERBB3	RAF1	CCL22	PEN	CMFB	TB4R2	L188P	CD8A	L9R	HCRI	CYP2F1	IFPI	PTCH2	CALCRL	CCR9 vA	CCR9 vB	S0CS1	CADPS	ICEBERG.	GABRR1	NRF	SCN7A	ADRAZA	NFKBIL1	NYREN18	CRZ	NFRKB
0.223529412	0.22333333 1	 -	0.222777778 E	0.222	0.222 (T	0.22055556	0.219411765	0.219333333 (0.218333333		0.218333333 (_	_	$\overline{}$	1	1	1	0.215555556	1	0.214	0.213888889	0.213888889	0.213529412	_	0.212352941	I	
0	0						0			0		0		, ,					0			 							

FIG.11-33A

0.2	0.16	0.17	0.29	0.16	0.1	0.23	0.21	0.32	0.27	0.22	0.26	0.27	0.3	0.19	0.32		0.18	0.18	0.28	0.26	0.21	0.28	0.14	0.14	0.21	0.18	0.21	0.16	0.18
0.25	0.22	0.23	0.24	0.22	0.14	0.27	0.3	0.27	0.75	0.24	0.39	0.23	0.19	0.28	0.3	0.16	0.21	0.21	0.33	0.19	0.24	0.21	0.22	0.14	0.23	0.18	0.22	0.13	0.19
0.32	0.24	0.16	0.3	0.14	0.1	0.37	0.5	0.26	0.41	0.23	0.31	0.22	0.33	0.23	0.3	0.17	0.23	0.23	0.22	0.22	0.26	0.19	0.15	0.21	0.27	0.19	0.24	0.29	0.21
0.34	0.37		0.51	0.5	0.12		0.28	0.39	0.3	0.29	0.37	0.3	0.51	0.29	0.3	0.18	0.22	0.22	0.36	0.25	0.5	0.33	0.7	1.83	0.33	0.24	0.47	0.16	0.23
0.23	0.34	0.27	0.22	0.21	0.14	0.24	0.21	0.27	0.39	0.25	0.31	0.26	0.24	0.22	0.36	0.7	0.23	0.23	0.5	0.27	0.32	0.7	0.21	0.24	0.24	0.5	0.27	0.28	0.17
	0.32		0.32	0.31	0.34	0.25	0.29	0.47	0.34	0.29	0.23	0.32	0.37	0.21	0.33	0.12			0.56	0.23	0.37	0.32	0.48	0.32	0.34	0.27	0.37	0.14	0.18
0.12	0.5	0.27	0.18			0.17	0.12	0.1	0.12		0.08	0.18	0.09	0.19	0.16	0.14	0.21	0.21	0.14	0.21	0.14		0.22	0.05	0.12	0.13	0.5	0.2	0.11
0.18	0.16	0.14	0.16	0.18	0.28	0.23	0.18	0.18	0.25	0.14	0.22	0.2	0.16	0.23	0.1	0.24	0.19	0.19	0.14	0.17		0.15	0.13	0.09		0.23		0.21	0.33
0.15	0.21	0.13	0.28	0.21	0.13	0.25	0.17	0.18	0.27	0.21	0.24	0.22	0.28	0.27	0.14	0.26	0.29	0.29	0.15	0.19	0.17	0.19	0.19	0.09	0.19	0.19	0.16	0.19	0.29
0.17	0.19	0.11	0.12	0.18	0.43	0.17	0.14	0.21	0.21	0.25	0.21	0.15	0.12	0.23	0.11	0.17	0.19	0.19	0.12	0.1	0.11	0.21	0.12	0.06	0.14	0.15	0.1	0.14	0.29
0.15	0.2	0.2	0.25			0.17	0.18	0.13	0.12		0.14	0.13	0.1	0.17	0.13	0.16	0.17	0.17	0.2	0.27	0.16		0.3	0.08	0.16	0.15	0.14	0.17	0.16

FIG 11-33R

		Γ-	_			ī	_	γ	Τ	_	T	1	<u> </u>	<u> </u>	_								_	_		_			
0.39		0.18	0.27	0.07	0.24	0.2	0.17		0.18	0.18	0.19	0.07	0.25	0.19	0.23	0.26	0.15	0.19	0.13	0.18	0.24	0.24	0.27	0.21	,	0.17	0.17	0.17	0.13
0.3	0.21	0.35	0.26	0.17	0.22	0.2	0.27	0.32	0.21	0.17	0.14	0.3		0.22	0.22	0.21	0.27	0.18	0.3	0.23	0.21	0.21	0.22	0.29	0.27	0.18	0.18	0.18	0.27
0.15	0.26	0.2	0.07	0.03	0.24	0.33	0.22	0.13	0.33	0.23	0.12	0.1	0.07	0.24	0.21	0.18	0.15	0.15	0.26	0.43	0.28	0.28	0.19	0.51	0.09	0.12	0.12	0.12	0.08
0.21	0.19	0.19	0.07	0.03	0.34	0.35	0.35	0.15	0.33	0.19	0.15	0.1	0.08	0.17	0.21	0.21	0.2	0.24	0.44	0.23	0.32	0.32	0.13	0.29	0.12	0.18	0.18	0.18	0.11
0.25	0.3	0.27	0.2	0.11	0.38	0.12	0.19	0.14	0.24	0.22		0.22	0.28	0.32	0.3	0.26	0.48	0.11	0.13	0.19	0.32	0.32	0.11	0.19	0.18	0.4	0.4	0.4	0.23
0.22	0.17	0.34	0.28	0.08	0.16	0.13	0.23	0.14	0.14	0.15	0.2	0.34	0.12	0.2	0.15	0.14	0.15	0.15	0.2	0.15	-0.16	0.16	0.1	0.12	0.28	0.22	0.22	0.22	0.22
0.23	0.19	0.3	0.29	0.06	0.13	0.13	0.22	0.17	0.12	0.17	0.24	0.19	0.08	0.2	0.15	0.12	0.16	0.14	0.26	0.17	0.15	0.15	0.1	0.12	0.24	0.22	0.22	0.22	0.24
																												1	
×-							~2						٧į	~	-		٨١	Αρ	v2		٧١	٧2		ط.		۷]	v2	۲3	
		0.21 HSPA1	0.20944444 NR3C	4444 CD3C	0.20944444 UBP1	0.20944444 CMKLR	11765 SLC1A3	0.208666667 CYP2S1	77778 IL 1RL 1	47059 IL10	_	2222 TH		38889 HMOX2	0.203888889 ZNF16	0.203529412 HTR3A	0.203333333 ANXA6	0.202777778 GABARAP	52941 AKAP9	0.201764706 TGFB1	36667 CYP19	0.201666667 CYP19 v2		0.2 IL 18RAP		17059 NR112	17059 NR112	0.197647059 NR112	2222 [CP1
0.2105			0.2094	0.20944444	0.2094	0.2094	0.209411765	0.2086	0.20777778	0.207647059	0.207647059	0.20722222	0.2070	0.203888889	0.2038	0.2035;	0.2033.	0.2027,	0.202352941	0.2017	0.201666667	0.2016			0.1993.	0.197647059	0.197647059	0.19764	0.19722222
				لــــــــــــــــــــــــــــــــــــــ								<u> </u>			ليــــ				لــــــــــــــــــــــــــــــــــــــ		ــــــــــــــــــــــــــــــــــــــ			ب_					

700	0.74	0.0	0.0	0.75	0.35	0.0	21.5	0.77	0.27	000	0.70	0.77	0.27	120	0 0	0 17	0 18	0.0	0.7	0.13	7 0	0.1	0.22	0.11	0.16	0.14	0.14	0.14	0.16
0 14	4.00	0.21		0.14	0.30	0.17	0 18	0.10	0.16	0.15	0.70	23.0	0.20	0.14	0.17	2	76.0	0.22	77.0	0.22	0.16	0.16	0.0	0.12	0.19	0.23	0.23	0.23	0.2
0.17		0.13	0.12	0.10	120	0.15	0.13	0.14	0.31	0.37	0.25	0.0	0.75	0.18	0.14	0 10	0.74	0.24	0 11	0.0	0.11	0.11	0.17	0.11	0.2	0.18	0.18	0.18	0.19
0 18	0.17		0.78	0.68	0.75	0.48	0.23	0.19	0.25	0.34	0.3	0.26	9.0	0.0	0.79	0.3	0.27	0.21	0.19	0.22	0.39	0.39	0.23	0.2	0.19		ī		0.37
0.17	0.2	0.1	0.19	0.34	0.15	0.24	0.21	0.22	0.3	0.28	0.28	0.22	0.23	0.21	0.22	0.21	0.2	0.4	0.12		0.12	0.12	0.3	0.13	0.24	0.2	0.5	0.2	0.18
0.2	0.28		0.22	0.43	0.26	0.28		0.31	0.24		0.25	0.35	0.32	0.28	0.21	0.28	0.25	0.31	0.22	0.18	0.18	0.18	0.39	0.3	0.27	0.2	0.2	0.2	0.52
0.2		0.26	0.75	0.04	0.22	0.22	0.25		0.5	0.19	0.17	90.0	0.17	0.19	0.13	0.17	0.14	0.15	0.25	0.22	0.19	0.19	0.16	0.3		0.15	0.15	0.15	0.17
0.2	0.26	0.18	0.18	0.12	0.5	0.15	0.19	0.28	0.11	0.16	0.15	0.17	0.11	0.14	0.12	0.22	0.17	0.24	0.15	0.14	0.16	0.16	0.18	0.14	0.5	0.21	0.21	0.21	0.07
0.16	0.27	0.25	0.23	0.12	0.17	0.2	0.22	0.27	0.16	0.16	0.21	0.2	0.26	0.17	0.16	0.23	0.18	0.21	0.19	0.24	0.17	0.17	0.21	0.17	0.16	0.27	0.27	0.27	0.15
0.15	0.16	0.2	0.24	0.07	0.12	0.12	0.14	0.19	0.1	0.12	0.2	0.25	0.09	0.17	0.17	0.14	.0.11	0.16	0.19	0.16	0.15	0.15	0.7	0.11	0.2	0.16	0.16	0.16	0.09
0.23		0.25	0.28	0.07	0.18	0.19	0.23		0.19	0.25	0.2	0.05	0.19	0.27	0.27	0.17	0.11	0.14	0.2	0.15	0.22	0.22	0.77	0.18		0.13	0.13	0.13	0.17

FIG.11-34B

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LC)
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				_	_			Γ-	Γ						Γ															_
0.1	0.23	0.24	0.23	0.16	0.28	0.15		0.12		0.24	0.14		0.1	0.16	0.09	0.17	0.19	•	0.13	0.13	0.13	0.13	0.07	0.18	0.2	0.16	0.5	0.13	0.21	0.22
0.37	0.25	0.34	0.28	0.21	0.21	0.28	0.23	0.2	0.27	0.22	0.18	0.3	0.26	0.28	0.14	0.18	0.27	0.2	0.29	0.3	0.3	0.3	0.15	0.24	0.2	0.24	0.17	0.27	0.25	0.23
0.08	0.34	0.15	0.26	0.09	0.42	0.09	0.22	0.07	0.09	0.43	0.05	0.16	0.08	0.26	0.26	0.08	0.18	0.21	0.34	90:0	90:0	90.0	0.04	0.08	0.17	0.22	0.14	0.1	0.23	0.11
0.07	0.27	0.21	0.18	0.13	0.23	0.09	0.5	0.07	0.15	0.33	0.07	0.24	0.07	0.27	0.21	0.08	0.17	0.16	0.29	0.08	0.08	0.08	0.08	0.1	0.21	0.14	0.16	0.11	0.21	0.1
0.2	0.3	0.31	0.14	0.19	0.23		0.11	0.13		0.22		0.25	0.17	0.18	0.15	0.1	0.13	0.16	0.34	0.21	0.21	0.21	0.12	0.12	0.18	0.28	0.11	0.14	0.16	0.28
0.15	0.25	0.2	0.19	0.13	0.15	0.13	0.14	0.15	0.13	0.15	0.09	0.21	0.18	0.19	0.11	0.23	0.17	0.13	0.19	0.21	0.21	0.21	0.07	0.17	0.18	0.16	0.16	0.14	0.13	0.19
0.13	0.26	0.23	0.17	0.1	0.16	0.11	0.5	0.12	0.28	0.11	0.07	0.15	0.16	0.17	0.11	0.21	0.15	0.16	0.16	0.23	0.23	0.23	90:0	0.14	0.16	0.11	0.12	0.07	0.13	0.2
PRV1	SPCB	LC22A5	PER2 v1	ABAT	CYP4F12	TAF9 v2	Sd8491	SCAP1	POR	INWI	BBOX1	SNX6 V1	PE	.PT2	RLF1	LDH3A2	.058	CYP8B1	SRRB	AIF1 v1	AIF1 v2	IF1 v3	ANXA3	RH1	NXA5	SLC1A2	TCF8	NFKB2	PSMB9 v1	CEBPA
0.19722222 F	0.197058824 HSPCB	0.197058824 SLC22A5	0.196875 F	0.196111111 A	$\overline{}$	0.194705882 1			0.194285714 F	0.193888889 SNW	0.193529412 E	192941176	0.192777778 CPE	0.1925 CPT2	191764706 (0.19055556 ALDH3A2	0.19 CD58	0.19 (0.19 ESRRB	0.188888889	0.188888889 A	0.188888889 AIF1	0.18875 4	0.188333333 HRH1	0.188235294 ANXAE	0.187222222 S		_		0.186470588 C
0.	0	0		0.	0.	0.	0	0	0.	0	0	0	0		0.	0	·			0.	0.	0		0	0	0.	0	0	0	0

0.11 0.46 0.28 0.10
0.25
0.1 0.36
0.12 0.23 0.17 0.13 0.19 0.13 0.27 0.3
0.35
0.09 0.33
0.23
0.27 0.14
0.15 0.58
0.27 0.13
0.1 0.61
0.2
0.13 0.31
0.1 0.2
0.2
0.25
0.18 0.18
0.12 0.46
0.46
0.46
0.05 0.14
0.05 0.36
0.25 0.25
0.19 0.17
0.22 0.22
0.06 0.31
0.26

FIG.11-35B

	_	_	Τ		_	-			_	_			Γ												_	_	_	_	
0.12	0.21	0.16		90:0	0.13	0.07	0.08	0.1	0.19	0.19	0.16	0.15	0.15	0.19	0.29	0.12	0.12	0.12	0.1	0.14	0.14	0.13		0.14	0.13	0.2	0.2	0.7	0.19
0.3	0.2	0.29		0.16	0.24	0.15	0.25	0.23	0.24	0.24	0.18	0.23	0.23	0.21	0.22	0.24	0.24	0.24	0.34	0.27	0.17	0.2	0.22	0.18	0.2				0.19
0.12	0.21	0.08		0.12	0.11	0.03	0.09	0.08	0.25	0.25	0.15	0.09	0.09	0.17	0.15	0.15	0,15	0.15	0.07	0.16		0.1	0.08	0.18	0.21	0.21	0.21	0.21	0.11
0.11	0.24	0.08		0.1	0.12	0.04	0.08	0.08	0.12	0.12	0.11	0.12	0.12	0.14	0.17	0.13	0.13	0.13	0.07	0.12	0.18	0.09	0.05	0.21	0.32	0.15	0.15	0.15	0.13
0.16	0.24	0.19		0.09	0.5	0.11	0.14	0.13	0.1	0.1	0.5	0.27	0.27	0.24	0.24	0.29	0.29	0.29	0.13	0.14	0.13	0.21	0.14	0.12	0.18	0.25	0.75	0.25	0.18
0.15	0.11	0.15		0.1	0.5	0.07	0.09	0.14	0.11	0.11	0.14	0.19	0.19	0.15	0.14	0.14	0.14	0.14	0.14	0.18	0.17	0.09	0.13	0.16	0.15	0.14	0.14	0.14	0.41
0.13	0.07	0.15		0.14	0.11	90.0	80.0	0.14	0.09	0.09	0.15	0.18	0.18	0.2	0.14	0.13	0.13	0.13	0.23	0.17	0.17	0.1	0.16	0.19	0.16	0.11	0.11	0.11	0.21
		0.183529412 GABBR1 v2	NRG1 vHRG-			0.182777778 HLA-00B1						0.18055556 NRG1 vGGF	0.18055556 NRG1 vHRG-beta3	0.18 BSG	0.18 INFRSF14	0.178823529 CASP10 v1	.:: 0.178823529 CASP10 vC	0.178823529 CASP10 vD	0.17777778 1.2	0.1775 AVPR1A	0.1775 CYT19	0.177222222 INFRSF17	0.177058824 GRM4	0.176875 GNRHR				0.175882353 CYP3A43 v3	0.175 TLR8 v1

FIG.11-36A

0.17	0.17	0.26	0.0	0 18	282	0.16	0.22	0.13	0.13	0.24	0.16	0.16	0.12	0.11	0.14	0.14	0.14	0.16	0.17	0.11	0.22	0.26	0.2	0.11	0.14	0.14	0.14	0.14
0.25	0.28	0.18	α. α.	0.0	0.68	0.3	0.23	0.27	0.27	0.15	0.13	0.13	0.22	0.17	0.17	0.17	0.17	0.2		0.23	0.28	0.22	0.18	0.17	0.12	0.12	0.12	0.15
0.23	0.31	-	7£ U	0.25	0.39	0.29	0.34	0.14	0.14	0.24	0.2	0.2	0.14	0.12	0.25	0.25	0.25	0.2	0.18	0.14	0.26	0.2	0.2	0.1	0.18	0.18	0.18	0.12
	0.22	0.29	15.0	0.42	0.32	0.58	0.44	0.35	0.35	0.32	0.16	0.16	0.22	0.27	0.37	0.37	0.37	0.38	0.28	0.31	0.46	0.27		0.18	0.27	0.27	0.27	0.21
0.32	0.25	0.26	0.28	0.22	0.36	0.28	0.33	0.21	0.21	0.19	0.17	0.17	0.18	0.14	0.23	0.23	0.23	0.26	0.16		0.27	0.21		0.16	0.15	0.15	0.15	0.18
		0.27	0.21	0.76	0.25	0.39	0.27	0.34	0.34	0.3	0.38	0.38		0.23				0.26	0.21	0.31	0.31	0.22	0.27	0.29	0.27	0.27	0.27	0.22
0.1	0.25	0.07	0.12	0.09	0.05	90.0	90:0	0.15	0.15	0.13	0.16	0.16	0.21	0.19	0.13	0.13	0.13	90.0	0.12	0.19	0.08	0.11	0.07	0.18	0.19	0.19	0.19	0.11
0.19	0.1	0.21	0.24	0.15	0.07	0.11	0.16	0.16	0.16	0.15	0.13	0.13	0.14	0.16	0.15	0.15	0.15	0.15		0.12	0.11	0.17	0.2	0.14	0.1	0.1	0.1	0.15
0.34	0.08	0.21	0.29	0.18	0.13	0.14	0.14	0.18	0.18	0.15	0.16	0.16	0.18	0.17	0.14	0.14	0.14	0.19	0.14	0.2	0.1	0.24	0.21	0.2	0.16	0.16	0.16	0.15
0.14	0.09	0.16	0.22	0.11	0.07	0.09	0.11	0.14	0.14	0.14	0.16	0.16	0.15	0.12	0.11	0.11	0.11	0.17	0.23	0.13	80:0	0.15	0.22	0.15	0.11	0.11	0.11	0.13
0.12	0.1	0.11	0.14	0.12	. 0.06	0.08	0.08	0	0	0.1	0.21	0.21	0.2	0.21	0.15	0.15	0.15	0.00	0.1/	0.14	0.0	7.0	0.1	0.14	0.24	0.24	0.24	0.1/1

FIG.11-37A

		_	_	_												_		T	T				T -	_	_	_			
0.19	0.15	0.18	0.13	0.18	0.15	0.14	0.23	0.23	0.27	0.14	0.15	0.18	0.14	0.19	0.17	0.14	0.15	0.19	0.1	0.17	0.17	0.18	0.11	0.19	0.13	0.13	0.12	0.18	0.13
0.19	0.27	0.22	0.2	0.21	0.2	0.14	0.2	0.2	0.22	0.22	0.39	0.26	0.18	0.21	0.21	0.2	0.32	0.22	0.18	0.24	0.24	0.28	0.22	0.2	0.19	0.3	0.19	0.18	0.3
0.11	0.1	0.16	90.0	0.16	0.13	0.13	0.1	0.1	0.18	0.12	0.1	0.21	0.09	0.08	0.18	0.05	0.18	0.19	0.07	0.11	0.1	0.1	0.1	0.12	0.19	0.21	0.14	0.09	0.14
0.13	0.11	0.23	0.1	0.16	0.13	0.08	0.07	0.07	0.15	0.09	0.12	0.22	0.1	0.08	0.13	0.05	0.13	0.18	0.05	0.17	0.11	0.1	0.11	0.19	0.44	0.14	0.12	0.1	0.11
0.18	0.5	0.21	0.16	0.24	0.09	0.12	0.1	0.1	0.13	0.18	0.19	0.26	0.12	0.12	0.11	0.15	0.14	0.28	0.14	0.26	0.32	0.31	0.14	0.17	0.17	0.24	0.17	0.26	0.17
0.41	0.19	0.17	0.17	0.13	0.13	0.18	0.16	0.16	0.12	0.13	0.21	0.16	0.16	0.17	0.19	0.14	0.21	0.18	0.13	0.21	0.15	0.18	0.18	0.17		0.19	0.14	0.13	0.18
0.21	0.19	0.18	0.12	0.16	0.11	0.14	0.15	0.15	0.1	0.16	0.22	0.15	0.12	0.21	0.17	0.13	0.19	0.16	0.12	0.16	0.16	0.13	0.11	0.16	0.09	0.16	0.11	0.13	0.14
0.175 TLR8 v2	. I	0.174117647 ADM	-		0.172777778 EREG		1					0.172222222 MMP8				0.170555556 TRHDE		0.17 C5	0.16944444 TRO v2	0.16944444 MS4A7		_	0.168823529 SYP		0.168235294 HSPC228	- 1	~ I.	0.166111111 AHR	0.16555556 CYP26A1 v1
:																					١		١	ارد		ا	ار		٠

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0.14	0.11	0.31	0.16	0.19	0.35	0.18	0.2	0.2	0.14	0.17	0.08	0.11	0.15	0.18	0.14	0.13	0.0	0.11	0.27	0.1	0.15	0.11	0.18	0.16	0.11	0.17	0.26	0.17	0.11
0.15	0.18	0.16	0.2	0.18	0.15	0.11			0.15	0.19	0.11	0.12	0.31	0.23	0.23	0.21	0.12	0.11	0.24	0.1	0.3	0.00	0.33	0.7	0.15	0.1	0.18	0.14	0.17
0.12	0.14		0.11	0.19	0.14	0.12	0.19	0.19	0.16	0.18	0.11	0.15	0.18	0.17	0.13	0.7	0.09	0.14	0.35	0.13	0.13	0.14	0.22	0.15	0.17	0.2	0.21	0.14	0.15
0.21	0.3	0.14	0.49	0.22	0.17	0.49	0.27	0.27	0.11	0.29	0.18	0.18	0.3	.0.33	0.7	0.42	0.18	0.17	0.2	0.21	0.21	0.16		0.24	0.19	0.17	0.2	0.38	0.23
0.18	0.13	0.12	0.21	0.15	0.13	0.13	0.36	0.36	0.41	0.26	0.12	0.17	0.23	0.25	0.18	0.21	0.13	0.13	0.19	0.1	0.15	0.1	0.15	0.16	0.15	0.13	0.22	0.12	0.24
0.22	0.21	0.23	0.45	0.31	0.37	0.31	0.18	0.18		0.21	0.16	. 0.17	0.21	0.29		0.52	0.17		0.3	0.29	0.22	0.44	0.22	0.21	0.21		0.29	0.27	0.15
0.11	0.21	0.12	0.1	0.18	0.28	0.07	0.08	0.08	90.0	0.04	0.7	0.18	0.12	0.13	0.14	0.07	0.17	0.19	0.11	0.17	0.12	0.19	0.12	0.13	0.17	0.12	0.15	0.14	0.09
0.15	0.18	0.12	0.1	0.14	0.11	0.21	0.17	0.17	0.5	0.25	0.15	0.12	0.19	0.13	0.19	0.1	0.2	0.13	0.21	0.16	0.13	0.1	0.27	0.12	0.12	0.15	0.14	0.13	0.19
0.15	0.16	0.14	0.12	0.14	0.12	0.23	0.19	0.19	0.21	0.22	0.23	0.16	0.18	0.16	0.21	0.13	0.22	0.16	0.17	0.15	0.12	0.14	0.19	0.17	0.18	0.18	0.16	0.15	0.21
0.13	0.17	0.13	0.11	0.04	0.18	0.21	0.14	0.14	0.18	0.16	0.2	0.12	0.14	0.1	0.19	0.09	0.21	0.12	0.14	0.15	0.14	0.09	0.12	0.13	0.1	0.08	0.08	0.12	0.16
0.17	0.14	0.14	0.12	0.14	0.17	0.12	0.14	0.14	0.14	0.00	0.18	0.18		90.0	0.14	0.13	0.17	0.23	0.08	0.17	0.13	0.2	 -:	0.16	0.1	0.17	0.12	0.16	0.11

FIG.11-38A

		_													_	_	T		Т	T		Г		_	_	_	,		
			L	L									<u>L</u>																
0.13	0.11	0.1	0.26	0.26	0.13	0.15	0.18	0.28	0.22	0.12	0.16	0.16	0.16		0.12	0.11	0.16	0.13	0.18	0.11	0.08	0.7	0.15	0.11	90.0	0.1	0.13	0.22	0.28
0.3	0.18	0.22	0.15	0.15	0.25	0.19	0.18	0.2	0.22	0.28	0.19	0.19	0.19	0.23	0.21	0.2	0.19	0.17	0.2	0.22	0.18	0.19	0.24	0.22	0.2	0.22	0.21	0.5	0.24
0.14	0.1	0.14	0.18	0.18	0.19	0.21	0.13	0.09	0.17	0.08	0.12	0.12	0.12	0.08	0.1	0.08		0.14	0.1	0.07	0.07	0.11	0.09	0.11	0.11	0.08	0.09	0.21	90.0
0.11	90.0	0.18	0.14	0.14	0.16	0.21	0.09	0.05	0.11	0.07	0.14	0.14	0.14	0.08	0.1	0.04	0.11	0.19	0.11	90.0	0.09	0.13	0.1	0.11	0.08	90.0	0.09	0.23	0.08
0.17		0.27	0.14	0.14	0.17	0.15	0.12	0.11	0.19	0.17	0.18	0.18	0.18	0.17	0.17	0.13	. 0.62	0.18	0.17	0.11	0.12		0.16	0.28	0.11	0.09	0.18	0.13	0.19
0.18	0.12	0.15	0.13	0.13	0.16	0.14	0.16	0.13	0.19	0.12	0.16	0.16	0.16	0.12	0.12	0.12	0.13	0.15	0.13	0.09	0.08	0.12	0.18	0.16	0.09	0.1	0.09	0.16	0.13
0.14	0.11	0.13	0.1	0.1	0.18	0.14	0.17	0.1	0.19	0.1	0.12	0.12	0.12	0.22	0.13	0.08	0.14	0.11	0.14	0.08	0.08	0.13	0.09	0.14	0.09	0.14	0.15	0.15	0.17
CYP26A1 v2	H.	STXBP1	WSB1 v1	WSB1 v2	三	CCRL1	CYP27A1	VCOA4	SNT-1	IL22R	ATRN v1	ntrn v2	atrn v3	SCN5A	SLC18A1	PRKCE	INXA1	SP110 vB	(COA6	ICOS	語	ST13	SLC25A5	DRD1	L2RA	IC2R	AIM2	_	CABRB3 v2
0.16555556 CYP26A1	0.165294118 HAL	0.163888889					0.161111111 (0.160588235		0.160555556 /	0.160555556 ATRN v2	0.160555556	0.16 SCN5A	0.16 SLC18A	0.159411765 F		0.158235294 S	0.15777778 NCOA6		0.157222222	0.157058824 S			0.156666667	0.155882353 MC2R	0.15555556 A		0.15555556 0
0		0	0	0	0	0	0			0	0	0			• .		0	0	0	0	0	0		0	0	0	0	0	Ö

FIG. 11-38B

0.11	0.13	0.09	0.11	0.11	90.0	0.08	0.13	0.22	0.07	0.26	0.17	0.17	0.17	0.17	0.17	0.13	0.12	0.16	0.13	0.18	0.16	0.12	0.15	0.14	0.22	0.18	0.16	0.08	ac c
0.17	0.18	0.19	0.15	0.15	0.07	0.1	0.11	0.39	0.12	0.17	0.21	0.21	0.21	0.14	0.24	0.23	0.11		0.13		0.27	0.19		0.15	0.17	0.15	0.22	0.09	0 11
0.15	0.22	0.14	0.09	0.09	0.2	0.09	0.12		0.08	0.18	0.17	0.17	0.17	0.12	0.18	0.23	0.11	0.19	0.12	0.16	0.25	0.14	0.21	0.16	0.34	0.13	0.18	0.09	0.1
0.23	0.5	0.29	0.15	0.15		0.43	0.29	0.23	0.19	0.19	0.5	0.2	0.2	0.15	0.28	0.54	0.16	0.2	0.24	0.12	0.48	0.26	0.28	0.21	0.22		0.11	0.14	0.10
0.24	0.21	0.14	0.1	0.1	0.12	0.14	0.17	0.23	0.14	0.15	. ~0.15	0.15	0.15		0.15	0.24	0.12	0.15	0.15	0.19	0.28	0.16	0.17	0.14	0.7	0.19	0.19	0.11	0
0.15	0.34	0.23	0.15	0.15	0.13		0.23			0.26	0.21	0.21	0.21	0.3	0.34	0.27	0.18	0.39	0.29	0.21	0.27	0.16	0.22	0.28	0.48	0.3	0.27	0.08	0.18
0.00	0.07	0.13	0.39	0.39	0.23	0.1	0.12	0.12	0.18	0.08	. 0.1	0.1	0.1		0.12	90:0	0.13	0.15	0.17	0.05	0.07	0.2		0.08	0.11	0.00	0.14	0.5	0.21
0.19	0.12	0.17	0.22	0.22	0.18	0.16	0.16	0.13	0.15	0.37	0.15	0.15	0.15	0.13	0.1		0.08	0.07	0.14	0.76	0.11	0.14	0.1	0.14	0.08	0.15	0.13	0.15	0.13
0.21	0.14	0.14	0.1	0.1	0.23	0.17	0.18	0.07	0.17	0.12	0.2	0.2	0.2	0.15	0.11	0.11	0.13	0.17	0.13	0.03	0:03	0.11	0.13	0.18	0.12	0.47	0.14	0.15	0.18
0.16	0.12	0.13	0.22	0.22	0.16	0.18	0.23	0.07	0.14	0.1	0.14	0.14	0.14	0.18	0.03	90.0	0.08	0.04	0.12	0.12	0.07	0.1	0.07	0.11	0.07	0.17	0.16	0.14	0.13
0.11	0.1	0.11	0.16	0.16	0.15	0.11	0.13	0.15	0.7	0.07	0.12	0.12	0.12		0.15	0.08	0.13	0.	0.19	90.0	0.08	0.21	0.17	-:	0.07	0.08	0.16	0.27	0.24

	0.1	0.14	0.13		0.08	0.11	0.18	0.74	0.09	0.12	0.11	0.2		0.07	0.07	0.07	0.12	0.12	0.14	0.1	0.1	0.12				90.0				
	0.12	0.11	0.1	0.7	0.1	0.07	0.15	0.32	0.08	0.13	0.07	0.23	0.11	0.07	0.08	0.08	0.1	0.13	0.13	0.1	0.28			0.07	0.12	0.11	0.16	0.08	0.16	
0.18	0.18	0.2	0.18	0.16	0.33	0.23	0.22	0.15	0.22	0.16	0.21	0.19	0.22	0.19	0.18	0.18		0.19	0.28	0.22	0.18	0.17	0.14	0.16	0.21	0.18	0.25	0.16	0.18	
0.04	90:0	0.12	0.05	0.47	0.05	0.05	0.23	0.08	0.09	0.17	0.12	0.14	0.07	0.98	0.03	0.03	0.03	0.07	0.08	0.21	0.04	0.11	0.16	0.04	0.15	0.05		0.03	0.09	
0.08	0.05	0.09	0.03	0.09	0.05	0.03	0.28	0.09	0.03	0.15	0.11	0.14	0.07	0.03	0.04	0.04	0.04	0.1	0.08	0.18	0.09	0.18	0.15	0.04	0.1	0.03	0.08		0.09	Ϋ́
0.12	0.13	0.24	0.12	0.12	0.1	0.11	0.12	0.12	0.09	0.18	0.13	0.2	0.19	0.12	0.11	0.11		0.14	0.19	0.2	0.11	0.14	0.08	0.11	0.12	0.2	0.19	0.1	0.12	FIG.11-39A
0.11	0.24	0.14	0.13	0.08	0.19	0.14	0.12	0.08	0.19	0.12	0.15	0.13	0.16	0.08	0.1	0.1	0.08	0.2	0.15	0.14	0.2	0.12	0.12	0.09	0.12	0.13	0.15		0.14	FIG.
0.12	0.11	0.13	0.13	0.09	0.18	0.14	0.14	0.08	0.22	0.11	0.1	0.11	0.11	0.07	0.08	0.08	0.04	0.24	0.15	0.1	0.09	0.13	0.14	0.07	0.11	0.15	0.11	90.0	0.11	
0.15533333 INFRSF11A	1	0.15333333 CYP7B1	0.1527777781CD1D	0.151764706 HSPA9B	. 0.151764706 TGFB2	7) 0.151176471 STAT6		ŀ.,	7 0.150588235 ASIP	☐ 0.15055556 CYP3A5		규. 0.15055556 MBP		子 0.15 CYP1B1	Ti 0.15 ОРР8 v1	T 0.15 DPP8 v2	0.15 SCGB1A1	J 0.14944444 SNAP29	= 0.148333333 CTSC v1	TI 0.14777778 ANXA2	C 0.147058824 CHRNA1	29 0.147058824 MYC	0.146428571 EAT2	0.14625 CYP7A1	0.146111111 IL17BR	0.14555556 HCRTR1	0.144705882 MEF2C	0.144666667 CXCL13	· · 0.1444444 DUSP14	

SUBSTITUTE SHEET (RULE 26)

0.2	0.12	0.16	0.24	0.13	0.18	0.18	0.11	0.08	0.18	0.12	0.14	0.09	0.18	0.12	0.16	0.16	0.33	0.12	0.14	0.09	0.16	0.03	0.13	0.16	0.15	0.5	0.12	0.14	0.15	
0.22	0.17	0.11	0.22	0.19	0.13	0.25	0.16	0.11	0.13	0.15	0.16	0.11	0.21	0.09			0.28	0.15	0.12	0.13	0.19	0.16		0.21	0.12	0.18	0.18	0.26	0.15	
0.17	0.16	0.16	0.3	0.18	0.18	0.18	0.08	0.07	0.18	0.15	0.12	0.1	0.23	0.2	0.2	0.2	0.15	0.14	0.19	0.12	0.15	0.15	0.11	0.5	0.13	0.21	0.1	0.24	0.13	
0.21	0.47	0.28	0.21	0.08	0.28	0.21	0.15			0.2	0.19	0.5	0.1	0.14	0.52	0.52	0.25	0.3	0.5	0.22	0.17	0.29	0.19		0.18	0.31	0.14	0.53	0.22	
0.16	0.27	0.12	0.27	0.21	0.17	0.31	0.13	0.11	0.15	0.16	0.16	0.15	0.17	0.23	0.26	0.26	0.22	0.15	0.15	0.1	0.19	0.15	0.24	0.24	0.37	0.18	0.13	0.24	0.14	-39B
0.34	0.18	0.3	0.28	0.21				0.26	0.23	0.26	0.22	0.16	0.22	0.09	0.27	0.27	0.41	0.26	0.26	0.46	0.13	0.18	0.23	0.47	0.17	0.5	0.14		0.2	FIG.11-39B
	90:0	0.13	0.04	0.09	0.09	0.08	0.18	0.07	0.06	0.12	0.1	0.18	0.05	0.03	90:0	0.06	0.07	0.09	0.11	0.1		0.17		0.05	0.08	0.07	0.13	0.05	0.12	LL .
0.14	0.12	0.11	0.11	0.12	0.17	0.18	0.09	0.07	0.34	0.12	0.24	0.11	0.16	0.07	0.19	0.19	0.13	0.07	0.11	90.0	0.13	0.1	0.11		0.13	0.12	0.13	90.0	0.15	
0.12	0.11	0.11	0.11	0.08	0.13	0.18	0.14	0.08	0.15	0.15	0.25	0.16	0.13	0.08	0.12	0.12	0.08	0.11	0.11	0.08	0.13	0.13	0.15	0.28	0.15	0.15	0.22	0.09	0.19	
0.12	0.11	0.11	0.1	0.08	0.17	0.12	0.09	90:0	0.13	0.14	0.13	0.11	0.17	0.04	0.08	0.08	0.07	0.11	0.08	0.05	0.16	0.11	0.1	90.0	0.12	0.09	0.1	0.05	0.12	

																	•												
0.06	0.15	0.14	0.1	0.09	0.11	0.18	0.1	0.13	0.12	0.12	0.13	0.12	0.11	0.18	0.13			0.13	90.0	0.16	0.1	0.12	0.1	0.12		0.13	0.14	0.13	0.12
90.0	0.12	0.13	0.1	0.13	0.28	0.12	0.13	0.14	0.12	0.13	0.12	0.1	0.13	0.14	0.12			0.12	0.08	0.13	0.09	0.12	0.18	0.08		0.12	0.11	0.1	0.1
0.47	0.17	0.15	0.17	0.5	0.5	0.18	0.25	0.16	0.19	0.17	0.19	0.24	0.28	0.21	0.14	0.19	0.24	0.17	0.14	0.2	0.27	0.18	0.16	0.25	0.17	0.14	0.2	0.16	0.17
0.05	0.11	0.12	0.11	0.05	0.05	0.09	90.0	0.16	0.27	0.27	0.11	0.08	0.05	0.08	0.12		0.08	0.15	0.08	0.12	0.04	0.05	0.21	0.09	0.09	0.12	0.12	0.08	0.1
0.04	90.0	0.12	90.0	0.05	0.05	0.1	0.05	0.16	0.26	0.21	0.12	0.07	0.04	0.08	0.1	0.15	0.08	0.11	0.1	0.13	90:0	0.05	90.0	90.0	0.09	0.05	0.2	0.07	90.0
0.07	0.2	0.16	0.16	0.13	0.14	0.14	0.16	0.2	0.15	0.11	0.12	0.16	0.16	0.12	0.13	0.11	0.12	0.12	90.0	0.17	0.18	0.11	0.1	0.22	0.11	0.14	0.12	0.13	0.24
0.24	0.1	0.14	0.11	0.12	0.12	0.12	0.21	0.13	0.09	0.1	0.1	0.19	0.19	90.0	0.12	0.1	0.1	0.15	0.13	0.16	0.1	0.00	0.1	0.19	0.1	0.1	0.12	0.12	0.15
0.22	0.07	0.12	0.11	0.04	0.07	0.07	0.18	0.15	0.08	0.11	0.09	0.15	0.2	0.07	0.12	0.14	0.14	0.09	0.09	0.14	0.08	0.08	0.09	0.16	0.13	0.1	0.12	0.1	0.11
PLA2R1	TNFRSF4	ZNF259	SCAP2	IMM	SFRS5	CCR4	 	CCL20	FB1	CCR2 vA	CHRNA4	CZMB	CXCL14	CASP8 vE	0.14 ALDH1A3	CYP2C18	DEFA4	IL12A	SGKL v1	ADIR	GRM7	NOC	SELE	CSF1	DCNP1	CHRNA7	ALDH1A1	PILR(ALPHA)	TNFRSF8 v1
0.143888889	0.143888889	0.143888889	0.143333333	0.142777778	0.142777778	0.14222222	0.14222222	0.141666667	0.141176471	0.141176471	0.141176471	0.141176471	0.14111111	0.140625	0.14	0.139285714	0.139285714	0.138888889	0.138888889	0.13875	0.138333333	0.13777778	0.13722222	0.136875	0.136666667	0.136470588	0.136111111	0.135294118	0.134705882
			; ; ;:	· .			<u> </u>	IR	<u>_</u> _	-1-	-1.	T		SI	HF	=	T	/F		l E	F 1	26	\	:			·	·	

FIG. 11-40B

0.09	0.00	0.12	0.12	0.16	0.18	0.15	0.12	0.08	0.1	0.09	0.1	0.11	0.1	0.16	0.14	0.11	0.14	0.12	0.15	0.1	0.11	0.16	0.12	0.11	0.13	0.22	0.11	0.16	0.13
0.1	0.11	0.16	0.23	0.26	0.13	0.19	0.11	0.11		0.11	0.12	0.15	0.12		0.22	0.18	0.18	0.12	0.21		0.21	0.14	0.1	0.11	0.18	0.13	0.11	0.21	0.11
0.09	0.12	0.11	0.1	0.18	0.2	0.18	0.17	0.1	0.13	0.09	0.13	0.14	0.13	0.19	0.17	0.1	0.12	0.12	0.14	0.13	0.17	0.28	0.15	0.16	0.14	0.12	0.13	0.18	0.1
0.18	0.24	0.21	0.24	0.19	0.7	0.16	0.19	0.15	0.19		0.26	0.25	0.22	0.18		0.13	0.17	0.17	0.22		0.35	0.26	0.18		0.15	0.21	0.15		0.28
0.09	. 0.15	0.16	0.13	0.5	0.18	0.12	0.12	0.1	0.12	0.17		0.17	0.24	0.19	0.21	0.14		0.14	0.28	0.14	0.19	0.18	0.19	0.1	0.16	0.17	0.16	0.17	0.25
0.18	0.26	0.19	0.45	0.38	0.23	0.21	0.21	0.13	0.13	0.21	0.13		0.18	0.27	0.22	0.25	0.31	0.29	0.22	0.15	0.21	0.3	0.25		0.25	0.18	0.2	0.24	20
0.06	0.08	0.17	0.1	0.11	0.09	0.1	0.08	0.23	0.15	0.14	0.1	0.08	0.07		0.13			0.1	0.06	0.14	0.00	0.09	0.19	0.12		0.08	0.14	0.08	0.1
0.13	0.37	0.12	0.09	0.11	0.15	0.13	0.12	0.11	0.08	0.12	0.36	0.13	0.12	0.12	0.1	0.1	0.09	0.15	0.12	0.1	. 0.07	0.08	0.11	0.16	0.09	0.15	0.1	0.09	0.1
0.08	0.11	0.14	0.11	0.08	0.1	0.12	0.16	0.15	0.13	0.15	0.14	0.14	0.12	0.11	0.12	0.14	0.1	0.15	0.16	0.14	0.13	0.12	0.11	0.12	0.15	0.16	0.13	0.15	0.1
0.38	0.08	0.13	0.09	0.03	0.09	0.5	0.14	0.16	0.03	0.1	0.08	0.12	0.08	0.07	0.09	0.11	0.08	0.1	0.18	0.11	0.07	0.07	0.07	0.14	0.11		0.03	0.13	0.07

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0.12	0.15			90.0	0.08		0.0	0.12	0.12	0.1	0.08	0.07	0.19		0.08	0.1.	0.08	0.08	0.09	0.09	0.11		0.11	0.1	0.12	0.08	0.07	0.07	0.11
0.18	0.17	0.19	0.18	0.17	0.18	0.24	0.17	0.2	0.22	0.2	0.5	0.16	0.19	0.18	0.14	0.19	0.17	0.17	0.24	0.17	0.18	0.18	0.16	0.17	0.19	0.2	0.17	0.15	0.7
0.00	0.1	0.05	0.08	0.03	0.1	0.08	0.15	0.05	0.08	0.09	0.08	0.03	0.13	0.12	0.04	0.07	0.07	0.04	0.08	0.05	0.07	0.05	0.1	0.04	0.14	0.09	90.0	0.04	0.11
0.07	0.11	0.05	0.08	0.03	0.07	0.09	0.14	0.04	0.11	0.13	0.06	0.04	0.12	0.09	0.04	0.07	0.06	0.04	0.08	0.05	90.0	0.04	0.1	0.03	0.16	0.12	0.03	0.04	0.08
0.1	0.11	0.12	0.1	0.08	0.2	0.1	0.09	0.11	0.22	0.15	0.17	0.13	0.14	0.07	0.11	0.11	0.1	0.15	- 0.14	0.11	0.12	0.14	0.19	0.11	0.5	0.14	0.11	90.0	0.16
0.14	0.12	0.1	0.09	0.1	0.13	0.15	0.08	0.1	0.13	0.15	0.13	0.08	0.11	0.07	0.07	0.11	0.15	0.1	0.13	0.13	0.14	0.08	0.13	0.07	0.11	0.15	0.12	0.07	0.11
0.11	0.11	0.15	0.14	0.07	0.12	0.13	90.0	0.1	0.12	0.14	0.13	0.08	0.16	0.11	0.07	0.03	0.1	0.11	0.00	0.1	0.1	0.14	0.11	0.04	0.1	0.07	0.08	0.04	0.09
0.13444444 KLRB1	0.13444444 TNFSF18		0.134 TNFRSF10C	0.133529412 IFNA8	0.133333333 CYP21A2	0.1325 LCK		0.131111111 PACE4	0.130625 GRM2	0.13 IL13RA1	0.13 11.9	0.12944444 CYSLTR1	. 0.129444444 NP	0.129333333 GFRA2	0.128235294 AR	0.12 <i>7777778</i> KIT	0.12 <i>777777</i> 8 CD4	0.127222222 DAP	0.127222222 LHCGR	0.125882353 IRF6	0.125882353 TNFSF8	0.124666667 TAC3	0.12444444 EPS15R	_ 1	0.124117647 CACNB4	0.122941176 ALDH4A1	0.122 <i>777778</i> AANAT	0.122777778 CDV-1	0.121666667 TBX21

FIG.11-41A

0.1	0.15	0.13	0.14	0.16	0.12	0.11	0.1	0.16	0.07	0.09	0.14	0.12	0.09	0.12	0.1	0.13	0.13	0.16	0.11	0.14	0.11	0.22	0.09		0.11	0.12	0.16	0.09	0.09
0.171	0.09	0.2	0.16	0.29	0.11	0.14	0.13	0.2		0.13	0.15	0.22	0.12	0.16	0.18	0.1	0.13	0.16	0.13		0.16	0.13	0.1	0.33	0.11	0.15	0.14	0.08	0.11
0.13	0.24	0.12	0.17	0.2	0.17	0.27	0.12	0.19	0.11	0.14	0.23	0.2	0.11	0.17	0.16	0.16	0.14	0.19	0.15	0.17	0.11	0.11	0.12	0.13	0.13	0.12	0.17	90:0	0.12
0.33	0.21	0.13	0.15	0.43	0.26	0.16	0.12	0.26		0.17	0.18	0.37	0.13	0.24	0.34	0.37	0.32	0.18	0.18	0.22	0.21	0.17	0.22	0.15	0.15	0.15	0.24	0.08	0.15
0.18	0.18	0.15	0.16	0.3	0.16	0.12	0.12	0.23	0.11	0.12	0.15	0.24	0.11	0.16	0.24	0.18	0.16	0.17	0.14	0.19	0.13	0.12	0.13	0.18	0.11	0.11	0.18	90:0	0.13
0.25	0.15	0.33	0.24		0.29	0.14	0.25	0.17	0.25			0.25	0.13	0.24	0.23	0.17	0.23	0.21	0.22	0.23	0.22	0.24	0.17			0.18	0.21	0.44	0.18
0.1	0.11			90.0	0.06	0.07	90.0	90.0	0.12	0.12	0.07	0.04	0.12		0.05	0.07	0.07	0.07	0.08	0.09	0.08		0.08	0.06	0.09	0.05	0.07	0.62	0.12
0.08	0.09	0.09	0.11	0.07	0.09		0.23	0.09	0.11	0.09	0.11	0.07	0.1	0.07		0.03	0.11	0.1	0.11	0.03	0.1	0.03	0.1	0.4	0.1	0.13	0.12	0.1	0.1
0.1	0.12	0.11	0.1	0.09	0.1	0.14	0.28	0.12	0.14	0.14	0.11	0.1	0.13	0.07	0.11	0.11	0.12	0.18	0.13	0.13	0.15	0.07	0.13	90:0	0.11	0.03	0.13	0.08	0.12
0.09	0.08	0.03	0.11	0.07	0.07	0.12	0.13	0.07	0.07	0.11	0.1	90:0	0.12	0.07	0.14	0.09	0.08	0.07	0.08	0.09	0.09	0.09	0.07	90.0	0.03	0.14	0.08	0.03	0.08
0.11	0.13			90.0	0.09	90.0	90.0	0.08	0.1	0.14	0.12	0.07	0.13		0.08	0.03	0.08	0.11	0.11	0.03			0.13	90.0	0.09		: 0.07	0.04	0.13

FIG.11-41B

FIG.11-42A

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0.1	0.07	0.11	0.11	0.1	0.12	0.13	0.11	0.08	0.07	0.11	0.11	0.12	0.15	0.13	0.11	0.07	0.13	0.11	0.07	0.08	0.13	0.03	0.08		0.07	0.19	90.0	0.1	0.15
0.18	0.5	0.19	0.16	0.14	0.15	0.16	0.17	0.17	0.15	0.18	0.16	0.19	0.18	0.18	0.19	0.17	0.17	0.16	0.18	0.22	0.21	0.16	0.17		0.5	0.12	0.5	0.18	0.16
0.05	. 0.03	0.06	0.08	0.04	0.08	0.11	0.07	0.1	0.03	0.08	0.05	0.12	0.08	0.04	0.13	0.04	0.07	0.11	0.04	90.0	- 0.1	0.08	0.07	90.0	0.09	0.22	0.05	0.07	90:0
0.06	0.04	0.07	0.07	0.05	0.11	0.1	0.08	0.07	0.03	90.0	90.0	0.12	0.08	0.04	0.12	0.03	0.1	0.12	0.03		0.1	0.09	0.05	0.06	0.05	0.13	0.05	0.07	0.04
0.14	0.11	0.14	0.14	0.08	0.12	0.08	0.17	0.18	0.18	0.09	0.14	0.13	0.1	0.13	0.08	0.1	0.14	0.19	0.08	0.08	0.1	0.15	0.12	0.09	0.08	0.13	0.12	0.15	0.07
0.15	0.07	0.1	0.1	0.12	0.13	0.1	0.16	0.09	0.09	0.19	0.1	0.11	0.15	0.07	0.1	0.13	0.08	0.09	0.1	0.12	0.1	0.09	0.09	0.09	0.16	0.09	0.09	0.12	0.07
0.14	0.07	0.11	0.03	0.1	0.09	0.08	0.09	0.05	0.07	0.1	0.09	0.11	0.13	0.05	0.11	0.09	0.07	0.07	0.09	0.12	0.1	0.09	0.07	0.12	0.11	0.07	0.08	0.1	0.09
C8B	IL13RA2	DMCDH	HTR1D	SCP2	IL23A	CATA3 .	DAPK1	NTT73	INST 9	GABRA4	HSPE1	LEC2	PHIP	CSF2RA v1	ALDH6A1	ITGA4	, CTN	301	(GBP1			MAP3K2	INFRSF6 v1		PTPRK	CYP51	BTK	TNFSF4	MDM2 vA
0.12125	0.120588235	0.120555556	0.120555556	0.120555556	0.12	0.11944444 GATA3	0.11944444	0.119375	0.118888889	0.118823529	. 0.118333333	0.118333333	0.118333333	0.117647059	0.117222222 ALDH6A	0.116666667	0.116666667	0.116470588	0.116111111	0.115625	0.115	0.114705882	0.114705882	0.114285714	0.114117647	0.114	0.113888889	0.113333333	0.112352941

FIG. 11-42B

90.0	0.12	0.11	0.08	0.12	0.11	0.11	0.08	0.18	0.11	0.13	0.08	0.1	0.08	0.13	0.00	0.12	0.08	0.09	0.2	0.1	0.06	0.1	0.1	0.12	0.13	0.07	0.1	0.08	0.00
	0.22	0.12	0.13	0.15	0.12	0.18	0.14		0.18	0.15	0.12	0.1	0.12	0.25	0.1	0.12	0.11	0.11	0.14		0.1	0.17	0.18	0.13	0.16		0.16	0.1	0.09
0.1	0.22	0.14	0.15	0.17	0.11	0.12	0.1		0.14	0.13	0.12	0.09	0.09	0.13	0.09	0.13	0.12	0.09	0.2	0.09	0.1	0.12	0.18	0.12	0.15	0.09	0.14	0.1	
0.18		0.18	0.21	0.22	0.15	0.19	0.18	0.16	0.36	0.7	0.27	0.15	0.19	0.19	0.12	0.24	0.19		0.2	0.1	0.15	0.16		0.13	0.5		0.25	0.18	0.11
	0.26	0.14	0.12	0.16	0.1	0.14	0.12	0.16	0.13	0.11	0.14	0.11	0.1	0.15	0.11	0.18	0.16	0.13	0.17	0.13	0.00	0.15	0.19	0.18	0.15	0.09	0.17	0.12	0.11
0.14	0.3	0.18	0.19	0.34	0.17	0.15	0.15	0.21	0.22		0.21	0.16	0.13		0.34	0.28	0.75	0.21	0.27	0.19	0.15		0.22	0.27		0.1	0.5	0.15	0.14
0.1	0.04	0.09	0.11	90.0	0.09	0.1	0.09	0.09	0.03	0.08	0.09	0.1	0.09	0.1	0.07	0.04	0.07	0.1	0.04	0.05	0.08	0.1	0.07		0.05	0.1	0.05	0.07	0.11
0.12	0.07	0.11	0.1	0.07	• 0.1	0.12	0.13	0.1	0.1	0.09	0.07	0.1	0.09	0.13	0.08	0.1	0.09	0.08	0.08	0.19	0.19	0.08	0.03	0.08	0.07	0.03	0.08	0.11	0.16
0.18	0.11	0.13	0.13	0.1	0.19	0.09	0.14	0.11	0.1	0.13	0.09	0.13	0.13	0.07	0.1	0.09	0.12	0.16	0.09	0.14	0.11	0.11	0.12	90.0	0.12	0.12	0.1	0.14	0.19
0.14	0.05	0.09	0.08	0.08	0.03	0.08	0.09	0.09	0.08	0.1	0.1	0.03	0.09	0.08	0.09	90.0	0.07	90.0	0.05	0.11	0.1	0.07	0.05	0.09	0.08		0.00	0.12	0.1
0.1	0.07	0.1	0.12	0.07	0.13	0.11	0.08	0.07	0.07	. 0.09	0.13	0.1	. 0.15	0.13	0.11	0:1:	0.08	0.1	0.06	0.07	0.1	0.14	0		0.07	0.1	0.07	0.08	0.17

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0.06	90.0	0.09	0.11	0.09	0.08	0.08	0.05	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.08	0.16	0.1	0.08			0.08	0.11	0.09	0.13	0.09	90.0	0.07	0.15	0.12
0.2	0.5	0.19	0.18	0.15	0.17	0.18	0.27	0.19	0.19	0.19	0.19	0.19	0.16	0.18	0.17	0.14	0.18	0.16	0.17	0.17	0.23	0.21	0.15	0.14	0.15	0.16	0.15	0.21	0.17
0.05	0.05	0.12	0.07	0.4	0.05	0.05	0.08					0.08	0.04	0.08	0.03	0.14	0.1	0.04	0.08	0.08	0.03	0.05	0.06		0.08	0.09	0.05	0.05	0.07
0.03								·	.05	.05	.05			,					0.02										,
								,																					
0.14		0.12							0.09										90.0										
0.19	0.19	0.11	0.1	0.0	0.2	0.08	0.12	0.08	0.08	0.08	90.08	0.12	0.08	0.11	0.08	0.08	0.1	0.0	0.07	0.07	0.11	80:0	0.09		0.08	0.07	0.1	90.0	0.1
0.13	0.13	0.00	0.11	0.04	0.16	90.0	0.1	90'0	90:0	90.0	90.0	0.09	0.1	0.1	0.07	0.07	0.11	0.08	0.12	0.12	0.11	0.05	0.07	0.12	0.07	90.0	0.08	0.07	0.08
															v1				1-1	1-2									
CASP6 va	CASP6 vb	CDX1	CYP39A1	GIOT-3	GPR58	SCN1B	NPY1R	MME v1	MME v1bis	MME v2a		FY	IFNAR1	SLC6A5	TNFRSF10B	GRIA4	IL7R	IRS4	CYP2C8 vHp1	CYP2C8 vHp1	TFRC	HAVCR2 -	EPHX2	CCL25 v2	TLR3	IFNGR1	AIG-1	GSTM3	CCR6 v1
0.11222222	0.112222222	0.112222222	0.112222222	1.11222222	0.111666667	0.111666667	0.111176471	0.110588235	0.110588235	0.110588235	0.110588235	0.11	0.11	0.11	0.11	0.108823529	0.108823529	0.108823529	0.108666667	0.108666667	0.108333333	0.108333333	0.107222222	0.106875	0.106470588	0.106111111	0.106111111	0.105882353	0.105555556
												<u> </u>										Ŀ							

FIG.11-43A

0.08	0.08	0.15	0.08	0.07	0.09	0.12	0.09	0.18	0.18	0.18	0.18	0.1	0.09	0.11	0.07	0.08	0.11	0.11	0.1	0.1	0.11	0.19	0.13	0.1	0.07	0.03	0.1	0.09	0.09
0.11	0.11	0.12	0.08	0.14	0.09	0.13		0.18	0.18	0.18	0.18	0.09	0.16	0.1	0.13	0.07	0.08	0.16	0.11	0.11	0.1	0.13	0.12	0.11	0.12	0.1	0.16	0.11	0.1
0.1	0.1	0.14	0.08	0.07	0.11	0.1	0.1	0.17	0.17	0.17	0.17	0.13	0.11	0.13	0.09	0.07	0.1	0.11	0.09	0.09	0.13	0.09	0.16	0.1	0.11	0.39	0.13	0.14	0.13
0.14	0.14	0.13	0.12	0.1	0.12	0.19	0.09	0.13	0.13	0.13	0.13	0.16	0.2	0.17	0.16	0.14	0.15	0.24	0.1	0.1	0.18	0.18	0.15	0.09	0.16	0.09	0.22	0.17	0.23
0.09	0.09	0.12	0.21	0.18	0.09	0.24	0.09	0.12	0.12	0.12	0.12	0.1	0.15	0.12	0.15		0.13	0.25	0.19	0.19	0.1	0.13	0.16	0.14	0.12	0.08	0.12	0.11	0.14
0.22	0.22	0.13	0.13	0.26	0.16	0.13	0.16	0.17	0.17	0.17	0.17	,	0.25			0.1			0.21	0.21	0.2	0.19	0.7	0.17	0.16	0.13	0.21	0.13	0.14
0.05	0.05	0.07	0.11	0.03	0.08	0.05	0.09	0.05	0.05	0.05	0.05	0.17	90:0	0.07	0.42	0.07	0.09	90:0			90:0	0.05	0.05	90.0	0.11	0.08	0.05	0.05	0.05
0.1	0.1	0.1	0.08	0.12	0.11	0.08	0.12	0.12	0.12	0.12	0.12	0.08	0.0	0.13	0.07	0.08	0.09	0.08	0.11	0.11	0.09	0.12	0.1	0.12		0.09	90.0		0.1
0.14	0.14	0.1	0.12	90:0	0.13	0.14	0.18	0.08	0.08	0.08	0.08	0.11	0.1	0.1	0.1	0.1	0.1	0.09	0.09	0.09	0.1	0.08	0.1	0.1	0.13	0.08	0.08	0.08	0.08
0.12	0.12	90:0	0.08	0.07	0.12	90:0	0.16	0.07	0.07	0.07	0.07	0.08	0.06	0.09	0.05	0.07	0.1	0.07	0.11	0.11	0.1	0.08	0.09	0.09	0.11	0.07	90.0	0.07	0.06
0.07	0.07	0.08	0.11	0.05	0.09	0.12	0.05	0.05	0.05	0.05	0.05	0.1	0.09	0.1	0.07	0	0.12	0.07			0.1	0.07	0.07	0.05	0.08	0.03	0.07	0.1	0.08

FIG. 11-43B

G.11-44A

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90:0	0.08	0.07	0.07	0.07	0.1	0.09	0.1	0.07	0.09	0.24	0.07	0.07	0.08	0.03	0.11	0.13		0.12	0.13	0.11	0.07	0.07	0.07	0.03	0.05	0.12	0.00	0.06	0.00
0.18	0.18	0.17	0.17	0.17	0.5	0.21	0.16	0.13	0.18	0.14	0.13	0.13	0.19	0.18	0.16	0.11	0.14	0.27	0.13	0.16	0.13	0.13		0.21	0.15	0.15	*	0.16	0.17
0.07	90.0	0.08	0.08	0.08	0.04	0.07	0.07	0.06	0.04	0.04	0.04	0.04	0.07	0.05	0.05	0.1	0.03		0.07	0.08	90.0	90.0	0.08	0.1	0.03	0.05	0.08	0.03	0.02
0.07	0.05	0.14	0.14	0.14	0.04	0.04	0.08	0.08	0.04	0.03	0.03	0.03	0.05	0.05	0.04	0.12	0.05	0.07	0.05	0.05	90.0	90.0	0.07	0.02	0.03	0.04	0.05	0.04	0.02
0.08	0.13	0.08	0.08	90:0	0.11	0.16	0.09		0.1	0.15	0.07	0.07	0.13	0.13	0.21	0.08	20.0	9	0.1	0.08	0.12	0.12	0.08	0.08	0.08	0.03	0.13	0.09	0.14
0.12	0.1	0.08	0.08	0.08	0.00	0.1	0.08	0.12	0.11	90.0	0.07	0.07	0.12	0.09	0.1	90.0	0.07	0.07	0.07	0.07	0.09	0.09	0.08	0.07	0.16	0.12	0.1	0.07	0.1
0.11	0.09	0.04	0.04	0.04	0.05	0.14	0.08	0.06	60.0	0.05	0.04	0.04	0.1	0.09	0.08	90'0	0.08	0.05	0.07	0.05	0.07	0.07	0.09	0.04	0.09	0.07	0.07	0.07	0.08
HTR1E	CSF2RB		IFNA21	IFNA4	NPYSR	II 8KB		CYP4F11	IRAK4	N-PAC	NPR2 vL	NPR2 vS	RTN1	0.1 JAK2	NFATC3	MTNR1B	TNFRSF9	AKR1C3	YARS	CCR8	TRAF2 v1		93	CHRNB3	08G		MAPK8IP1	RFXAP	
0.105294118 HTR1	0.105294118	0.105	0 105	0.105	0 104375	0.102941176	0.10222222	0.101764706	0.101176471	0.101176471	0.101111111	0.10111111	0.100555556	0.1	0.1	0.09944444 MTNR1B	0.099375	0.098666667	0.0972222	0.096666667	0.096666667	0.096666667	0.09625	0.096111111	0.095555556	0.095555556	0.095333333	0.095294118	0.093888889
										-			<u> </u>	<u> </u>			<u> </u>							<u> </u>				<u> </u>	

0.1	0.11	0.1	0.1	0.1		0.1	0.08	0.08	0.07	0.03	0.08	0.08	0.09	0.08	0.08	0.08	0.14	0.1	0.08	0.07	0.1	0.1	0.11	0.09	0.08	0.06	0.09		0.03
0.1	0.13	0.13	0.13	0.13	0.12	0.11	0.1	0.14	0.21		9.0	0.0	0.07	0.09	0.11	0.1	0.13	0.1	0.16	0.13	0.09	0.09	0.11	0.14	0.08	0.08		0.08	0.12
0.09	0.13	0.09	0.09	0.09	0.07	0.07	0.08	0.1	0.08	0.06	0.09	0.09	0.1	0.1	0.09	0.09	0.14	0.1	0.1	0.00	0.12	0.12	0.1	0.1	0.12	0.07	0.1	0.08	0.1
0.17		0.1	0.1	0.1	0.15	0.07	0.5	0.19		0.12	0.09	0.09	0.12	0.16		0.16	0.18	0.09	0.13	0.13	0.18	0.18	0.19	0.12	0.11	0.33		0.14	0.13
0.12	0.14	0.11	0.11	0.11	0.09	0.09	0.1	0.12	0.09	0.1	90.0	90:0	0.11	0.11	0.11	0.1	0.17	0.11	0.09	0.1	0.12	0.12	0.11	0.1	0.09	0.1	0.13	0.08	0.1
	0.21	0.5	0.7	0.2	0.26		0.24	0.15	0.22	0.17	0.11	0.11	0.15	0.19	0.17	0.21	0.19		0.16	0.5	0.19	0.19	0.15	0.16	0.5	0.14	0.2	0.39	0.21
0.00	90.0	0.04	0.04	0.04		90:0	0.06	90.0	0.07	0.05	0.04	0.04	0.08	90.0	90.0	0.07	0.03	0.05	0.08	0.05	90.0	90.0	90.0	0.05	40:0	0.04	0.08	0.04	0.03
0.11	0.08	0.12	0.12	0.12	0.13	0.13	0.08	0.09	0.07	0.13	0.11	0.11	0.08	0.07	0.08	0.07	0.05	0.13	0.12	0.13	0.08	0.08		0.12	0.19	90:0	0.08	0.08	0.07
0.15	0.08	0.21	0.21	0.21	0.08	0.12	0.03	0.12	0.1	0.05	90.0	90.0	0.1	0.09	0.08	0.1	0.08	0.08	90.0	0.1	0.08	0.08	0.09	0.08	0.12	0.07	0.08	0.08	0.09
0.11	0.07	0.09	0.09	0.09	0.08	0.11	0.07	0.08	90:0	0.07	90:0	90.0	0.07	· 0.07	90:0	0.07	0.04	0.09	0.07	0.09	90:0	0.00	0.07	0.07	0.05	0.07	90.0	0.05	0.1
0.00	. 0.09	0.04	0.04	-0.04	90.0	0.08	0.08	0.08	0.1	0.17	.0.07	0.07	0.1	0.1	0.11	0.08		0.05	0.08	0.08	90.0	90.0	0.08	90.0	.0.05	90.0	0.09	0.08	90.0

FIG. 11-44B

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			T	Τ	Τ	T	T		Τ	Т	Γ	Γ	<u> </u>	<u> </u>	Γ	Γ	Γ											T		l
0.08	0.07	90.0	0.08	0.08	0.08	0.05	0.08	0.08	0.07	0.07	0.08	0.08	90.0	0.12	90.0	0.04	0.05	90.0	0.08	0.08	0.08	0.05	0.08	0.05		0.09	0.07	90:0	0.07	
0.13	0.16	0.14	0.16	0.15	0.19	0.13	0.14	0.13	0.17	0.17	0.14	0.14	0.14	0.14	0.16	0.15	0.16	0.13	0.18	0.16	0.17	0.15	0.17	0.11	0.13	0.15	0.17	0.13	0.15	
0.04	0.07	0.14	0.03	0.05	0.04	0.02	0.05	0.03	0.04	90:0	0.08	0.08	0.04	0.07	0.04	0.04	0.03	0.04	0.05	90.0	90.0	0.05	0.12	0.14	0.03	0.04	0.04	0.05	0.07	
0.04	0.09	0.11	0.03	0.05	0.03	0.02	0.04	0.04	0.03	0.07	0.05	0.05	0.03	90.0	0.03	0.02	0.03	0.03	0.03	0.04	0.05	0.04	0.05	0.07	0.02	0.04	0.03	0.04	0.05	
0.1	0.12	0.12	0.07	0.13	0.08	0.07	0.08	0.16	0.08	0.08	0.1	0.1	0.09	0.1	0.07		0.1	0.09	90.0	0.1	0.11	0.07	0.11	90:0	0.08	0.1	0.07	0.09	0.11	
90.0	90.0	0.07	0.08	0.07	0.09	90:0	0.08	0.08	0.1	0.09	90.0	90.0	0.08	0.07	0.09	0.06	0.08	0.07	0.08	0.07	0.08	0.08	0.06	90.0	0.05	0.08	90.0		0.08	•
0.05	0.03	0.07	0.08	90:0	0.08	90.0	0.08	0.09	0.08	0.1	0.07	0.07	0.07	0.09	0.07	90.0	0.07	0.06	90.0	0.04	0.07	0.06	90.0	0.03	0.08	0.08	0.05	0.00	0.08	i
GRM3	HTR4	339	HTR1B	JAM2	GPR57	CXCL9	NIS	IAN4L1	MD-2	RFRP	ALDH3B1	ALDH3B2	CAMLG	NR5A2	GADD45A	TACR1 vL	CD1C	TFP12	SNX4	IL16	ANXA4	CHRM2	NCOA6IP	CXCL11	121	NTF5	COASTER	IRAK3	ADRB2	
1 1	\sim		0.091666667		0.090588235		\neg						\neg	0.088823529	_		-		$\neg \neg$	1				_	_		$\overline{}$	0.084117647	0.08388889	
		اد	<u>.</u>	ا .	٠	;;		0			0	0	0	0	0	:	0	0	0	0	0	.	0	:-		0	0	0	2	

0.07
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0.05
0.08
0.1
90:0
0.09

FIG.11-45B

FIG.11-46A

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0.08	90.0	0.05	0.06		0.07	0.07	0.06	0.09	0.06	0.07	0.06	0.06	0.06	0.07	0.08	90.0	90.0	0.09	0.04	0.04	0.04	0.04	0.05	0.04	0.09	0.05	0.05	90.0	0.05
0.12	0.13	0.16	0.15	0.14	0.13	0.13	0.16	0.15	0.15		0.15	0.16	0.15	0.15	0.15		0.12	0.14	0.11	0.11	0.11	0.11	0.14	0.15	0.13	0.13	0.13	0.16	0.13
0.04	0.03	0.04	0.05	90.0	0.03	0.03	0.04	-0.04	0.04		0.03	0.03	0.05	0.04	90.0	0.05	0.03	0.03	0.03	0.03	0.03	0.03	0.04	0.02	90.0	0.05	0.03		0.03
0.04	0.02	0.04	0.04	0.04	0.03	0.03	0.02	0.04	0.03	0.04	0.02	0.02	0.04	0.03		0.05	0.02	0.04				0.03	0.03	0.02	0.04	90.0	0.03	0.02	0.03
0.06	. 0.09	0.09	. 0.08	0.09	0.08	0.08	0.03	0.00	0.07	0.09	0.07	0.09	0.1	0.09	0.11	0.09	0.12	0.08	0.05	0.05	0.05	0.09	90.0	0.08	0.08		90.0	90.0	0.08
0.05	0.09	80.0	0.08	0.07	0.07	0.07	0.08	0.08	0.06	0.09	0.07	0.08	0.08	0.08	0.07	0.08	0.07	0.09	0.05	0.05	0.05	0.08	0.05	0.08	0.04	90.0	0.05	90.0	90.0
0.04	90:0	90.0	0.07	0.07	0.06	90.0	0.07	0.07	0.05	0.07	0.09	90.0	0.07	90:0	90.0	0.07	0.07	0.07	0.03	0.03	0.03		0.04	0.05	0.05	0.05	0.03	0.03	90.0
									-1			7																	
Q	RGRP	1A	A5		vi	٧2	182	_			J				A1			١٨	۷1	۷ĵ	٧3	5A1 v2	SF11B						
0.08375 CABRQ	0.083529412 HSOBRGRP	0.082941176 MTNR1A	0.082777778 CABRA5	0.0825 L1RN	AF1	FAF1	4706 HSD11B2	0.081764706 TIMP4	1111 GAD2	0.080666667 STAT4	0.08 PDGFC	0.08 ZIC2	4444 BF	1765 115	0.078823529 BCL2A	0.078125 TD02	6875 LEPR	0.076470588 RORA v	2353 GH1	0.075882353 GH2 v1	0.075882353 GH2 v3	0.075 ALDH5A1	0.075 TNFRSF1	0.07444444 HRH4	4444 TBK1	0.074 A2M	0.073333333 GHITN	6471 Tar1	0.07055556 NR2E
0.08	0.08352	0.08294	0.08277	0.0	0.08	0.08	0.081764706	0.08176	0.081111111	0.08066			0.07944444	0.079411765	0.07882.	0.07	0.07	0.07647	0.07588	0.07588	0.07588	0	0	0.07444	0.07444444	0	0.07333	0.07117647	
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0.19	0.08	0.00	0.06		0.00	0.00	0.08	0.05	0.11	0.08	0.00	0.08	0.07	0.00	0.00	0.00	0.07	0.00	0.07	0.07	0.07	0.07	0.05	0.08	0.08		0.07	0.06	0.05
0.13		0.09	0.08	0.08	. 0.11	0.11	0.11	0.1	0.08	0.08	0.08	0.1	0.07	0.09	0.06	0.16		0.08	0.12	0.12	0.12		0.1	0.11	0.1	0.08	0.12	0.11	0.08
0.08	0.1	0.09	90.0	0.09	0.11	0.11	0.11	0.08	0.12	0.09	90:0	0.09	0.1	0.08	0.06	0.07		0.08	0.05	0.05	0.05	0.09	0.18	0.07	0.06	0.08	0.06	0.05	0.07
0.14	0.18	0.14	0.12	0.13				3	0.19		0.12	0.14	0.14	0.18	0.12		0.15	0.1	0.08	0.08	0.08	0.18	90.0	0.11	0.08	0.12	0.17	0.08	0.15
0.08	0.11	0.11	0.09	0.11	0.11	0.11	0.1	0.07	0.1	0.09	0.13	0.11	0.08	0.12	0.07	0.09	0.1	0.1	0.07	0.07	0.07	0.11	90.0	0.12	0.07	0.09	0.07	0.05	90:0
0.13	0.19	0.14	0.25	0.09	0.18	0.18	0.5	0.16	0.15	0.18	0.15	0.11	0.12		0.1	0.16	0.14		0.3	0.3	0.3	0.16	0.2	0.15	0.15	0.11	0.16	0.17	0.13
	0.04	0.04	0.04	90.0	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.05	90.0	0.07	0.05	0.04	90.0	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.04	0.04	0.03	0.04
	90.0	0.08	0.06	0.08			90.0	0.13	0.05	0.09	0.11	90.0	90.0	90.0	90.0	90.0	0.06	90:0	0.09	0.09	0.09	0.05	0.1	0.07	0.11	0.05	0.1	0.12	0.08
90.0	0.07		0.09	0.08	0.08	0.08	90:0	0.09	90.0	0.07	0.07	0.09	0.07	0.07	0.08	0.08	0.07	0.08	90:0	90.0	90:0	0.05	0.07	90:0	90:0	0.08	90.0	0.06	0.00
0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.00	0.08	0.05	0.07	0.05	0.05	0.05	0.05	90:0	0.04	0.04	0.04	0.03	90:0	0.04	0.07		0.05	90:0	0.05
0.05	90.0	90.0	0.05	0.08	90.0	90.0	90.0	90:0	90.0	0.07	0.05	0.07	0.05	90.0	0.08	0.07	90.0	0.08	0.07	0.07	0.07	0.05	0.03	0.00	0.04	90.0	0.04	0.03	0.00

FIG.11-46B

1] [5	5	4		1
0.0	0.07		0.0	0.05	0.0		0.07
0.11	0.15	0.11	0.14		0.13	0.14	0.12
0.06	0.03		0.03	0.04	0.03	0.02	0.03
0.03	0.03	. 0.02	0.03	0.03	0.02	0.02	0.02
0.09	0.09	0.07	0.07	90:0	90:0	90.0	0.07
0.06	90.0	90.0	0.07	0.05	0.05	90.0	0.05
0.06	0.07	0.04	90.0	0.03	90.0	90.0	0.05
0.07 ADRBK2	0.06944444 GPR48	0.068125 BRS3	0.068125 CCL7	0.06733333 IFITM1	0.066666667 PLG	0.064 TNFSF15	0.0525 PRX

FIG.11-47A

700	0.06	900		90.0		0.03	0.02	0.06	0.03	0.04
0.05	0.07			0.09	0.16	0.03	0.05	0.00	0.04	CS:
90.0	0.08	0.09	0.12	0.1	0.1	0.03	90.0	0.07	CS:	C: C:
	0.16	0.04	0.07	0.06	0.19		0.09	0.00	0.04	0.0 4.0
0.08	0.1	0.1		0.1		0.03	0.06	0.06	9). (C)	CO.O
90.0	0.08	0.07	0.14	0.11	0.13	50.0	0.05	0.00	C.S.	0.04
0.00	0.06	0.00	0.11	0.07	0.09	0.04	0.00	0.0	0.00	300
3	5	200		700	000	200	300	000	900	700
0.05	10	0.05	0.09	0.07	0.12	0.05	0.05	0.07		0.00
			i							- 00

FIG.11-47B

st differences in PNI gene expression using rank test	Accession # gene abbrev # > 0 # normal in first 4 # normal in last 4	4 sod1 0 3	3 CLC 12 0 3	3 GREB1 vo 12 0 3	3 ERBB2 3 0	7 (LAT 0 3		1 (CCL24 10 0 3	•					0 3 3 3 0	•	5 CCL28 v1 3 0	
most robust differences in	Accession #	NM_000454	NM_001828	NM_014668	NM_004448	NM_014387	NM_013447	NM_002991	NM_000460	NM_020984	NM_014369	NM_001781	NM_001335	NM_000620	NM_016166	NM_019846	

		Gene	THP0	PTPN1	-
significant in both rank test and parametric tests	(.01 level) (male only)	Accession #	NM_000460	NM_014369	****

Gene Abbreviation

Accession #

NM_001781

test and parametric tests (.1 level) (female only)

significant in both rank

69Q)

Accession #	Gene Abbreviation
NM_000460	1HPO
NM_014369	PTPN18
NM 000413	HSD17B1

FIG. 12-1

only late in adulthood exhibit very mild loss of motor neurons with resulting minor muscle weakness. *mice that are homozygous for an inactivated CNTF gene develop normally and initially thrive and

120/126

	fold difference	0.5	0.630057803	0.342995169	0.647058824	0.459677421	0.583007812	0.559210526	1,495798319	0.79318542	0.64619883	0.741830065	0.563917526	0.416030534	0.68076923	0.781609195	0.64375	0.763790665	1.369458131	1.37254902	0.788235294	0.780534351	1.308510638	0.604477612	0.773076923	0.560483871	1.593283582
	mean well	0.1	0.865	0.5175	0.3825	0.103333333	0.426666667	0.76	0.595	1.5775	0.4275	0.3825	1.2125	0.655	0.216666667	0.2175	0.2	0.2525	0.145	0.255	0.2125	1.31	0.235	0.1675	0.975	0.31	0.335
.:	mean sick	0.05	0.545	0.1775	0.2475	0.0475	0.24875	0.425	0.89	1.25125	0.27625	0.28375	0.68375	0.2725	0.1475	0.17	0.12875	0.192857143	0.198571429	0.35	0.1675	1.0225	0.3075	0.10125	0.75375	0.17375	0.53375
	Category 2	Immune: Cytokines/Chemokines	Transcription Factor	Immune: Complement Component	Immune: Cytokines/Chemokines	Neuronal: Neurotransmitter Receptor	Immune: Complement Component	mmune: Cytokines/Chemokines	Neuronal: Regulates Neurotransmitter Activity	Protease Inhibitor	Immune: Cytokine/Chemokine Receptors	Transcription Factor	Immune: Other Immune Function	Immune: Cytokines/Chemokines	Immune: Other Immune Function	Immune: Other Immune Function	Endocrine: Regulated by Hormones	Circadian	Immune: Other Immune Function	Neuronal: Neurotransmitter Receptor	Signal Transduction	Immune: Other Immune Function	Other Neruoendocrine Function	Immune: Other Immune Function	Endocrine: Hormone Metabolism	Immune: Regulates Cytokine Activity	Endocrine: Hormone Receptor
	Gene Abbrev	CXCL11	RFX2 v1	MASP v2	IL1F8	Tar1	ಬ	1.3	SYN3	CST3	CNTFR*	TFE3	6900	11.26	NYREN18	CD58	PSCD2	PER2	KPNB2	VIPR2	黑	돼	SGNE1	SELE	CYP2F8	IL18RAP	NR3C2
PNI genes	Accession#	U59286	NM_000635	XM_029606	AF200494	AF380185	NM_000064	NM_000588	NM_003490	00000_MN	NM_001842	NM_006521	NM_001781	NM_018402	NM_016118	NM_001779	NM_017457	NM_022817	NM_002270	NM_003382	NM_005546	NM_000460	NM_003020	NM_000450	NM_007253	NM_003853	NM_000901

SUBSTITUTE SHEET (RULE 26)

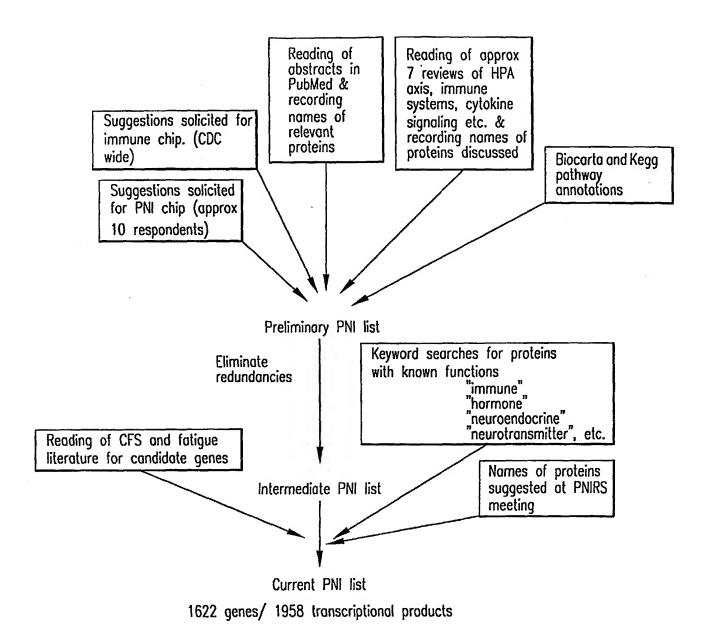
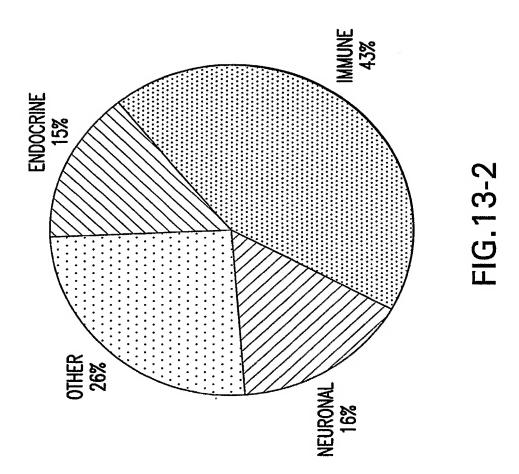
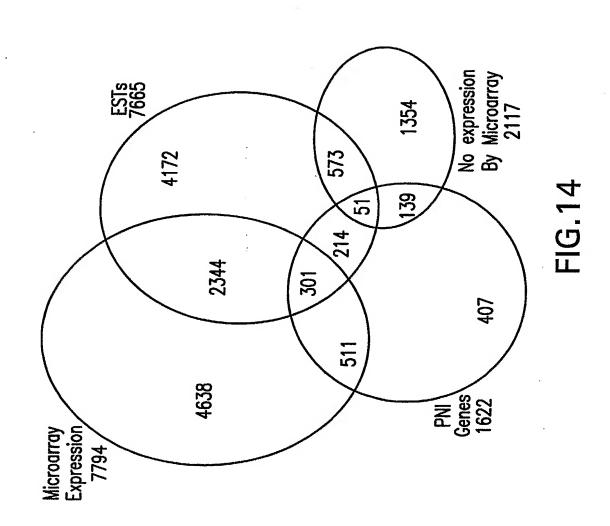
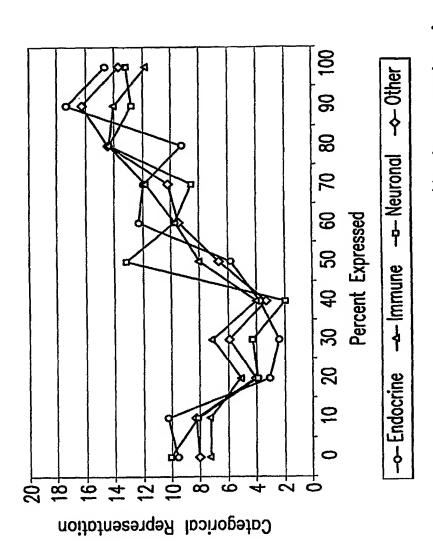


FIG. 13-1







Categorical Representation = Number of genes at that Percent Expressed Percent Expressed = Number of arrays evidencing expression of a given gene/Number of arrays for which data is available level/Number of genes in the category

Multivariate

Correlations				
	log2sARM NOMM1	log2sARM NOMM2	log2sARM NOMM3	
log2sARM NOMM1	1.0000	0.8109	0.7771	
log2sARM NOMM2	0.8109	1.0000	0.7931	
log2sARM NOMM3	0.7771	0.7931	1.0000	. •

3758 rows not used due to missing values.

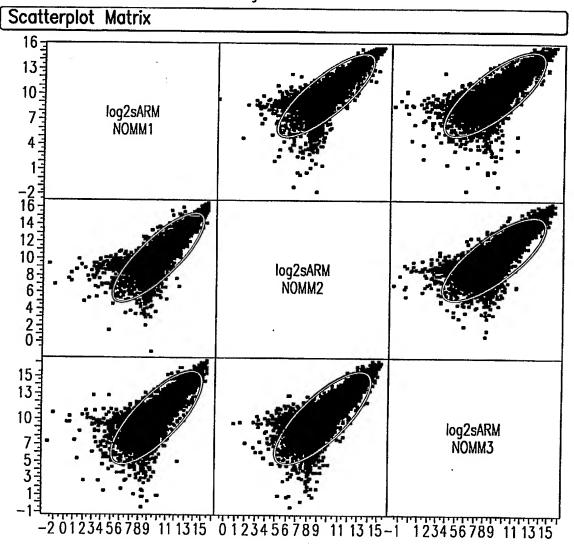


FIG. 16

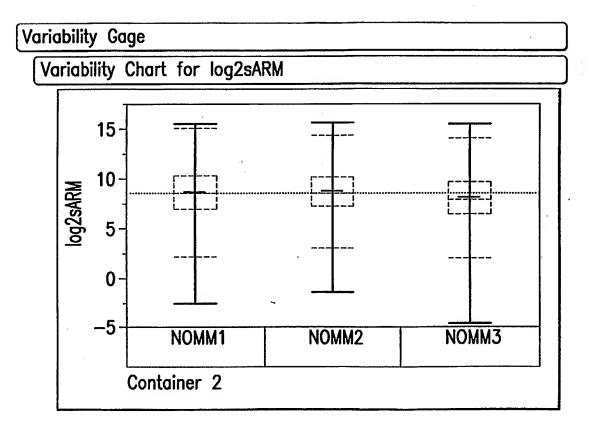


FIG.17